GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 14:57:06 ; Search time 8.69136 Seconds
(without alignments)
839.896 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1000	100.0	176	1	TR23_MOUSE	Q9er63 mus musculu
2	705	70.5	180	1	TR22_MOUSE	Q9er62 mus musculu
3	226.5	22.7	332	1	TNR6_PIG	O77736 sus scrofa
4	219.5	21.9	323	1	TNR6_BOVIN	P51867 bos taurus
5	215.5	21.6	454	1	TR1A_MOUSE	P25118 mus musculu
6	211.5	21.1	351	1	CRMB_COWPX	O73559 cowpox viru
7	210	21.0	461	1	TR1A_RAT	P22934 rattus norv
8	208.5	20.8	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
9	205.5	20.5	455	1	TR1A_HUMAN	P19438 homo sapien
10	205	20.5	327	1	TNR6_MOUSE	P25446 mus musculu
11	202.5	20.2	349	1	CRMB_VARV	P34015 variola vir
12	196	19.6	471	1	TR1A_BOVIN	O19131 bos taurus
13	194	19.4	324	1	TNR6_RAT	Q63199 rattus norv
14	193.5	19.4	461	1	TR1A_PIG	P50555 sus scrofa
15	189.5	18.9	335	1	TNR6_HUMAN	P25445 homo sapien
16	186	18.6	417	1	TR16_MOUSE	Q9z0w1 mus musculu
17	183	18.3	427	1	TR16_HUMAN	P08138 homo sapien
18	181	18.1	655	1	TR21_MOUSE	Q9epu5 mus musculu
19	175	17.5	655	1	TR21_HUMAN	O75509 homo sapien
20	171	17.1	425	1	TR16_RAT	P07174 rattus norv
21	168	16.8	283	1	TR14_HUMAN	Q92956 homo sapien
22	167.5	16.8	300	1	TR6B_HUMAN	O95407 homo sapien
23	167.5	16.8	326	1	VT2_MYXVL	P29825 myxoma viru
24	166.5	16.7	416	1	TR16_CHICK	P18519 gallus gall
25	164.5	16.4	386	1	T10D_HUMAN	Q9ubn6 homo sapien
26	164.5	16.4	417	1	TR12_HUMAN	Q93038 h tumor nec
27	164	16.4	325	1	VT2_SFVKA	P25943 shope fibro
28	162.5	16.2	381	1	T10B_MOUSE	Q9qzm4 mus musculu
29	161.5	16.2	259	1	T10C_HUMAN	O14798 h tumor nec
30	160.5	16.1	416	1	TR19_MOUSE	Q9j113 mus musculu
31	156	15.6	468	1	T10A_HUMAN	O00220 homo sapien
32	155	15.5	401	1	T11B_RAT	O08727 rattus norv
33	152	15.2	461	1	TR1B_HUMAN	P20333 homo sapien
34	150.5	15.0	415	1	TNR3_MOUSE	P50284 mus musculu
35	150	15.0	271	1	TNR4_RAT	P15725 rattus norv
36	150	15.0	401	1	T11B_MOUSE	O08712 mus musculu
37	150	15.0	435	1	TNR3_HUMAN	P36941 homo sapien
38	149	14.9	595	1	TNR8_HUMAN	P28908 homo sapien
39	148	14.8	250	1	TNR7_MOUSE	P41272 mus musculu
40	145	14.5	260	1	TNR7_HUMAN	P26842 homo sapien
41	145	14.5	474	1	TR1B_MOUSE	P25119 mus musculu
42	145	14.5	498	1	TNR8_MOUSE	Q60846 mus musculu
43	144	14.4	277	1	TNR4_HUMAN	P43489 homo sapien
44	144	14.4	401	1	T11B_HUMAN	O00300 homo sapien
45	140.5	14.1	493	1	TNR8_RAT	P97525 rattus norv

ALIGNMENTS

RESULT 1
TR23_MOUSE
ID TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
DE factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF1AL1 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Risser P.;
RT "Characterization of SOB, a member of the TNFR family.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC ---

CC ---
DR EMBL; AJ278264; CAC16405.1; -.
DR EMBL; AJ276505; CAC27352.1; -.
DR EMBL; AY046550; AAL05072.1; -.
DR HSSP; P19438; 1EXT.
DR MGD; MGI:1930269; Tnfrsf23.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).
FT REPEAT 37 72 TNFR-CYS 1.
FT REPEAT 74 114 TNFR-CYS 2.

```
FT   REPEAT      115    155       TNFR-CYS 3.
FT   DISULFID     38     49       BY SIMILARITY.
FT   DISULFID     50     63       BY SIMILARITY.
FT   DISULFID     53     72       BY SIMILARITY.
FT   DISULFID     75     90       BY SIMILARITY.
FT   DISULFID     93    106       BY SIMILARITY.
FT   DISULFID     96    114       BY SIMILARITY.
FT   DISULFID    116    131       BY SIMILARITY.
FT   DISULFID    134    147       BY SIMILARITY.
FT   DISULFID    137    155       BY SIMILARITY.
FT   CARBOHYD    148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   176 AA;  19594 MW;  EE30D617F49DDB7D CRC64;

  Query Match             100.0%;  Score 1000;  DB 1;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-75;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60

Qy      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120

Qy     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176


RESULT 2
TR22_MOUSE
ID   TR22_MOUSE     STANDARD;      PRT;   180 AA.
AC   Q9ER62; Q9CZA4; Q8VHB9;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis
DE   factor receptor p60 homolog 2) (TNF receptor family member SOBa).
GN   TNFRSF22 OR TNFRSF1AL2 OR TNFRH2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX   MEDLINE=20519229; PubMed=11063728;
RA   Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA   Lane N., Reik W., Walter J.;
RT   "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT   implications for a novel imprinting centre and extended imprinting.";
RL   Hum. Mol. Genet. 9:2691-2706(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Risser P., Mao W., Baldwin D.T., Pan G.;
RT   "Characterization of SOBa, a murine member of the TNFR family.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ278265; CAC16406.1; -.
DR   EMBL; AJ276505; CAC27353.1; -.
DR   EMBL; AY046551; AAL05073.1; -.
DR   EMBL; AK012838; BAB28502.1; -.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1930270; Tnfrsf22.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     41       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       42    180       EXTRACELLULAR (POTENTIAL).
FT   REPEAT       47     82       TNFR-CYS 1.
FT   REPEAT       84    124       TNFR-CYS 2.
FT   REPEAT      125    165       TNFR-CYS 3.
FT   DISULFID     48     59       BY SIMILARITY.
FT   DISULFID     60     73       BY SIMILARITY.
FT   DISULFID     63     82       BY SIMILARITY.
FT   DISULFID     85    100       BY SIMILARITY.
FT   DISULFID    103    116       BY SIMILARITY.
FT   DISULFID    106    124       BY SIMILARITY.
FT   DISULFID    126    141       BY SIMILARITY.
FT   DISULFID    144    157       BY SIMILARITY.
FT   DISULFID    147    165       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     12     12       L -> V (IN REF. 3).
FT   CONFLICT    171    180       RRSASVAWPI -> NPRNRLFLLL (IN REF. 2).
SQ   SEQUENCE   180 AA;  20226 MW;  F8F56E165ADD53FA CRC64;

  Query Match             70.5%;  Score 705;  DB 1;  Length 180;
  Best Local Similarity   79.9%;  Pred. No. 3e-51;
  Matches  131;  Conservative    5;  Mismatches   20;  Indels    8;  Gaps    1;

Qy       5 SHVSSLSHWF--------LLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG 56
           | ||||| ||        |||||||| | | ||| | :|| || ||| | ||||| | :|
Db       7 SLVSSLSRWFLWRRLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG 66

Qy      57 TFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC 116
           |||||||:||||||||||||||||| ||| |  | ||||||||| ||||||||||||:|
Db      67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126

Qy     117 QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 160
           : |||||||||||||||||||||||||||||||||||||||||||
Db     127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170


RESULT 3
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TNR6_PIG
ID   TNR6_PIG       STANDARD;      PRT;   332 AA.
AC   O77736;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001202; CAA04596.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    332       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 6.
FT   DOMAIN       17    175       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    176    192       POTENTIAL.
FT   DOMAIN      193    332       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       45     81       TNFR-CYS 1.
FT   REPEAT       82    125       TNFR-CYS 2.
FT   REPEAT      126    164       TNFR-CYS 3.
FT   DOMAIN      227    311       DEATH.
FT   DISULFID     46     57       BY SIMILARITY.
FT   DISULFID     58     71       BY SIMILARITY.
FT   DISULFID     61     80       BY SIMILARITY.
FT   DISULFID     83     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    141       BY SIMILARITY.
FT   DISULFID    144    155       BY SIMILARITY.
FT   DISULFID    147    163       BY SIMILARITY.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   332 AA;  37592 MW;  5B8B03682756BF1B CRC64;

  Query Match             22.7%;  Score 226.5;  DB 1;  Length 332;
  Best Local Similarity   29.9%;  Pred. No. 7.2e-12;
  Matches   43;  Conservative   28;  Mismatches   62;  Indels   11;  Gaps    5;

Qy      38 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTC 96
           ||:|:::    ||: || |    | | |    ||  |  |  :| |::    |  |  |
Db      46 CPEGQHREGQFCCQPCPPGKRKHADCTSPGGAPQCVPCSEGEDYTDKNHHSSKCRRCRVC 105

Qy      97 DKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTV 154
           | :  :  :  |: | : || |:   : :  :  | | ||| |  |  |:: |  |:||
Db     106 DGEHGLEVEKNCTRTQNTKCRCKPNFFCHTSQC-EHCNPCTTCEHG--VIENCTPTSNTK 162

Qy     155 C-----SSSVSNPRNWLFLLMLIV 173
           |     |:   :  :||: |::::
Db     163 CREVFQSAGSRSNLHWLWALLILI 186


RESULT 4
TNR6_BOVIN
ID   TNR6_BOVIN     STANDARD;      PRT;   323 AA.
AC   P51867;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96226401; PubMed=8634151;
RA   Yoo J., Stone R.T., Beattie C.W.;
RT   "Cloning and characterization of the bovine Fas.";
RL   DNA Cell Biol. 15:227-234(1996).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U34794; AAC48546.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
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```
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    323       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 6.
FT   DOMAIN       17    170       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    171    188       POTENTIAL.
FT   DOMAIN      189    323       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       45     80       TNFR-CYS 1.
FT   REPEAT       81    124       TNFR-CYS 2.
FT   REPEAT      125    163       TNFR-CYS 3.
FT   DOMAIN      238    306       DEATH.
FT   DISULFID     45     56       BY SIMILARITY.
FT   DISULFID     57     70       BY SIMILARITY.
FT   DISULFID     60     79       BY SIMILARITY.
FT   DISULFID     82     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    140       BY SIMILARITY.
FT   DISULFID    143    154       BY SIMILARITY.
FT   DISULFID    146    162       BY SIMILARITY.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   323 AA;  36445 MW;  4D88A90E9E1F4892 CRC64;

  Query Match             21.9%;  Score 219.5;  DB 1;  Length 323;
  Best Local Similarity   31.4%;  Pred. No. 2.6e-11;
  Matches   44;  Conservative   26;  Mismatches   63;  Indels    7;  Gaps    5;

Qy      37 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT-FTGKDNGLHDCELCST 95
           :| :| |: :  ||: || |      ||      :|  |  |  :| | :    |  ||
Db      44 SCQEGLYREHQFCCQPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTDKSHHSDKCIRCSI 103

Qy      96 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 153
           ||::  :  :  |: | : || |:   :: :    | | ||| |  ||  :::|  |:||
Db     104 CDEEHGLEVEQNCTRTRNTKCRCKSN-FFCNSSPCEHCNPCTTCEHGI--IEKCTPTSNT 160

Qy     154 VCSSSVSNPRN-WLFLLMLI 172
           |  | |:  : |  |::||
Db     161 KCKGSRSHANSLWALLILLI 180


RESULT 5
TR1A_MOUSE
ID   TR1A_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Bebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   EMBL; BC004599; AAH04599.1; -.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
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DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    454       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN      22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   213    235       POTENTIAL.
FT   DOMAIN     236    454       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     339    349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356    441       DEATH.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    195       BY SIMILARITY.
FT   DISULFID   185    191       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  0710C2E8C3C2B6D9 CRC64;

  Query Match             21.6%;  Score 215.5;  DB 1;  Length 454;
  Best Local Similarity   28.1%;  Pred. No. 7.3e-11;
  Matches   52;  Conservative   23;  Mismatches   61;  Indels   49;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |     | :|  ||||   | |  |  |
Db      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 103

Qy      95 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |: : |  : | |  |  | |   |   |  :  |   |  |: |  | |  |
Db     104 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN-----WLFLLML 171
           | ||||:                                ::|:||::     | |::|
Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVIL 220

Qy     172 IVFCI 176
           :  |:
Db     221 LGLCL 225


RESULT 6
CRMB_COWPX
ID   CRMB_COWPX     STANDARD;      PRT;   351 AA.
AC   O73559;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90 / Grishak;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "The genomic sequence analysis of the left and right species-specific
RT   terminal region of a cowpox virus strain reveals unique sequences and
RT   a cluster of intact ORFs for immunomodulatory and host range
RT   proteins.";
RL   Virology 243:432-460(1998).
RN   [2]
RP   FUNCTION.
RC   STRAIN=Brighton red;
RX   PubMed=8091665;
RA   Hu F.Q., Smith C.A., Pickup D.J.;
RT   "Cowpox virus contains two copies of an early gene encoding a soluble
RT   secreted form of the type II TNF receptor.";
RL   Virology 204:343-356(1994).
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; Y11842; CAA72578.1; -.
DR   EMBL; Y15035; CAA75306.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    351       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31     67       TNFR-CYS 1.
FT   REPEAT      69    110       TNFR-CYS 2.
FT   DISULFID    32     43       BY SIMILARITY.
FT   DISULFID    44     57       BY SIMILARITY.
FT   DISULFID    47     67       BY SIMILARITY.
FT   DISULFID    70     85       BY SIMILARITY.
FT   DISULFID    88    102       BY SIMILARITY.
FT   DISULFID    92    110       BY SIMILARITY.
FT   CARBOHYD   103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   351 AA;  38253 MW;  57CAE73EF4E5D7C7 CRC64;

  Query Match             21.1%;  Score 211.5;  DB 1;  Length 351;
  Best Local Similarity   38.7%;  Pred. No. 1.3e-10;
  Matches   48;  Conservative   14;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      38 CPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-T 95
           | | ||  :::|| :|| ||:    |    :|  ||  |  |||| ::| |  |  |:
Db      32 CKDNEYNRHNLCCLSCPPGTYASRLCDSKTNTNTQCTPCGSGTFTSRNNHLPACLSCNGR 91

Qy      96 CDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN 152
           || :|     |: | :| |||  | ||\  |    |: |   |||  |  |     || :
Db      92 CDSNQVETRSCNTTHNRICECAPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSTGD 149
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Qy    153 TVCS 156
          |||
Db    150 VVCS 153


RESULT 7
TR1A_RAT
ID   TR1A_RAT       STANDARD;      PRT;   461 AA.
AC   P22934; Q91V30; Q91Y93;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC   STRAIN=Various;
RA   Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT   among autoimmune susceptible and resistant inbred rat strains.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   EMBL; AF329976; AAK53562.1; -.
DR   EMBL; AF329977; AAK53563.1; -.
DR   EMBL; AF329981; AAK53567.1; -.
DR   EMBL; AF329978; AAK53564.1; -.
DR   EMBL; AF329979; AAK53565.1; -.
DR   EMBL; AF329980; AAK53566.1; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      363    448       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    185    191       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     230    230       I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                                 DA/BKL AND F344/NHSD).
FT   VARIANT     295    295       H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                                 DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FBD202 CRC64;

  Query Match             21.0%;  Score 210;  DB 1;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 2.1e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy     38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
          || |:|   ::| :||  |  ||:: : |  |  :  || |  ||||   | :  |  |
Db     44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCK 103

Qy     95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
          || |:  |  :: | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db    104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy    150 TANTVCS--------------------------------SSVSNPRN----------WL 166
            ||||:                                ::|:||::          :|
Db    161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy    167 FLLMLIVFCI 176
           | :|   ||
Db    221 GLCLLFFICI 230


RESULT 8
CRMB_CAMPS
ID   CRMB_CAMPS     STANDARD;      PRT;   349 AA.
AC   Q8UYA7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
```

```
OS   Camelpox virus (strain CMS), and
OS   Camelpox virus (strain M-96).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=203172, 203173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMS;
RX   PubMed=11907336;
RA   Gubser C., Smith G.L.;
RT   "The sequence of camelpox virus shows it is most closely related to
RT   variola virus, the cause of smallpox.";
RL   J. Gen. Virol. 83:855-872(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M-96;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA   Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT   "The genome of camelpox virus.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY009089; AAG37456.1; -.
DR   EMBL; AY009089; AAG37718.1; -.
DR   EMBL; AF438165; AAL73920.1; -.
DR   EMBL; AF438165; AAL73917.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31     65       TNFR-CYS 1.
FT   REPEAT      67    108       TNFR-CYS 2.
FT   DISULFID    32     43       BY SIMILARITY.
FT   DISULFID    44     57       BY SIMILARITY.
FT   DISULFID    47     65       BY SIMILARITY.
FT   DISULFID    68     83       BY SIMILARITY.
FT   DISULFID    86    100       BY SIMILARITY.
FT   DISULFID    90    108       BY SIMILARITY.
FT   CARBOHYD   101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  38064 MW;  EA412AF991E087F3 CRC64;

  Query Match             20.8%;  Score 208.5;  DB 1;  Length 349;
  Best Local Similarity   37.4%;  Pred. No. 2.2e-10;
  Matches   46;  Conservative   15;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      38 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 96
           | | ||: :::|| :|| ||:    |    |  ||  |  |||| ::| |  |  |: |
Db      32 CKDNEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 90

Qy      97 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 153
           | :|     |: | :| |||  | ||   |    |: |   |||  |  |     |  :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCILKGSSGCKACVSQTKCGIGYGVSGH-TSAGDV 148

Qy     154 VCS 156
           :||
Db     149 ICS 151


RESULT 9
TR1A_HUMAN
ID   TR1A_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor
DE   binding protein 1 (TBPI)].
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90235285; PubMed=2158863;
RA   Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA   Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90235284; PubMed=2158862;
RA   Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA   Tabuchi H., Lesslauer W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE=91006021; PubMed=1698610;
RA   Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA   Aderka D., Holtmann H., Wallach D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91017509; PubMed=2170974;
RA   Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT   expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250049; PubMed=1315717;
RA   Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
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RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 41-45.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX   MEDLINE=93258809; PubMed=8387891;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE=97094982; PubMed=8939750;
RA   Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
RN   [11]
RP   VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX   MEDLINE=99213501; PubMed=10199409;
RA   McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,
RA   Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA   Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA   Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
RA   Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA   Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
RA   Hitman G.A., O'Shea J., Kastner D.L.;
RT   "Germline mutations in the extracellular domains of the 55 kDa TNF
RT   receptor, TNFR1, define a family of dominantly inherited
RT   autoinflammatory syndromes.";
RL   Cell 97:133-144(1999).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis. Contributes to
CC       the induction of noncytocidal TNF effects including anti-viral
CC       state and activation of the acid sphingomyelinase.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- PTM: The soluble form is produced from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
CC       familial hibernian fever (FHF), a disease characterized by
CC       recurrent fever, abdominal pain, localized tender skin lesions and
CC       myalgia.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
DR   EMBL; M33294; AAA03210.1; -.
DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
DR   EMBL; A21522; CAA01558.1; -.
DR   EMBL; BC010140; AAH10140.1; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   Genew; HGNC:11916; TNFRSF1A.
DR   MIM; 191190; -.
DR   MIM; 142680; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Disease mutation; Polymorphism; 3D-structure.
FT   SIGNAL       1     21
FT   CHAIN       22    455       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A, MEMBRANE FORM.
FT   CHAIN       41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    455       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     338    348       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356    441       DEATH.
FT   DISULFID    44     58
FT   DISULFID    59     72
FT   DISULFID    62     81
FT   DISULFID    84     99
FT   DISULFID   102    117
FT   DISULFID   105    125
FT   DISULFID   127    143
FT   DISULFID   146    158
FT   DISULFID   149    166
FT   DISULFID   168    179

  Query Match            20.5%;  Score 205.5;  DB 1;  Length 455;
  Best Local Similarity  31.3%;  Pred. No. 4.8e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
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          | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 10
TNR6_MOUSE
ID   TNR6_MOUSE     STANDARD;      PRT;   327 AA.
AC   P25446; Q9DCQ1;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92148151; PubMed=1371136;
RA   Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
RA   Copeland N.G., Jenkins N.A., Nagata S.;
RT   "The cDNA structure, expression, and chromosomal assignment of the
RT   mouse Fas antigen.";
RL   J. Immunol. 148:1274-1279(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   Koczan D., Ibrahim S.M., Thiesen H.J.;
RT   "Role of a mutant fas receptor in a transgenic mouse.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE OF 1-96 FROM N.A.
RX   MEDLINE=93189576; PubMed=7680478;
RA   Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT   "Aberrant transcription caused by the insertion of an early
RT   transposable element in an intron of the Fas antigen gene of lpr
RT   mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN   [5]
RP   VARIANT LPR.
RX   MEDLINE=92195401; PubMed=1372394;
RA   Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA   Nagata S.;
RT   "Lymphoproliferation disorder in mice explained by defects in Fas
RT   antigen that mediates apoptosis.";
RL   Nature 356:314-317(1992).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC       LIVER, LUNG, HEART, AND ADULT OVARY.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC       DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC       PRODUCTION.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M83649; AAA37593.1; -.
DR   EMBL; AK002590; BAB22211.1; -.
DR   EMBL; AJ295702; CAC00638.1; -.
DR   EMBL; AJ295703; CAC00638.1; JOINED.
DR   EMBL; AJ295704; CAC00638.1; JOINED.
DR   EMBL; S56490; AAB25700.1; -.
DR   EMBL; S56485; AAB25700.1; JOINED.
DR   EMBL; S56486; AAB25700.1; JOINED.
DR   PIR; A46484; A46484.
DR   HSSP; P25445; 1DDF.
DR   MGD; MGI:95484; Tnfrsf6.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Disease mutation.
FT   SIGNAL       1     21
FT   CHAIN       22    327       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 6.
FT   DOMAIN      22    169       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   170    186       POTENTIAL.
FT   DOMAIN     187    327       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     79       TNFR-CYS 1.
FT   REPEAT      80    123       TNFR-CYS 2.
FT   REPEAT     124    162       TNFR-CYS 3.
FT   DOMAIN     222    306       DEATH.
FT   DISULFID    44     55       BY SIMILARITY.
FT   DISULFID    56     69       BY SIMILARITY.
FT   DISULFID    59     78       BY SIMILARITY.
FT   DISULFID    81     97       BY SIMILARITY.
FT   DISULFID   100    115       BY SIMILARITY.
FT   DISULFID   103    123       BY SIMILARITY.
FT   DISULFID   125    139       BY SIMILARITY.
FT   DISULFID   142    153       BY SIMILARITY.
FT   DISULFID   145    161       BY SIMILARITY.
FT   CARBOHYD    43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    246    246       I -> N (IN LPR).
FT   CONFLICT    38     38       H -> R (IN REF. 3).
SQ   SEQUENCE   327 AA;  37418 MW;  F6BFFC5ACE356EEE CRC64;
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  Query Match             20.5%;  Score 205;  DB 1;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 4.1e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy      37 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 95
           || :| ||    ||: |  |       ||:       |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      96 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 153
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     154 VCSSSVSNPRNWLFLLMLIVFCI 176
           |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 11
CRMB_VARV
ID   CRMB_VARV      STANDARD;      PRT;   349 AA.
AC   P34015; Q89098; Q85407; Q89118;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   CRMB OR G2R OR G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=India-1967 / Isolate Ind3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bangladesh-1975;
RX   MEDLINE=94088747; PubMed=8264798;
RA   Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA   Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA   Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA   Venter C.J.;
RT   "Potential virulence determinants in terminal regions of variola
RT   smallpox virus genome.";
RL   Nature 366:748-751(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966, and Somalia-1977;
RA   Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA   Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966;
RX   MEDLINE=20107289; PubMed=10639322;
RA   Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA   Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA   Esposito J.J.;
RT   "Alastrim smallpox variola minor virus genome DNA sequences.";
RL   Virology 266:361-386(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   EMBL; L22579; AAA60933.1; -.
DR   EMBL; U18339; AAA69407.1; -.
DR   EMBL; U18341; AAA69467.1; -.
DR   EMBL; Y16780; CAB54798.1; -.
DR   EMBL; U88146; AAB94371.1; -.
DR   EMBL; U88148; AAB94373.1; -.
DR   EMBL; U88149; AAB94374.1; -.
DR   EMBL; U88152; AAB94377.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; O14763; 1DOG.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     65       BY SIMILARITY.
FT   DISULFID     68     83       BY SIMILARITY.
FT   DISULFID     86    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    215    215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      17     17       MISSING (IN STRAINS BANGLADESH-1975 AND
FT                                CHIMP 9-4).
FT   VARIANT     160    160       H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT                                1966 AND SOMALIA-1977).
FT   VARIANT     165    165       A -> T (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     182    182       E -> K (IN STRAIN SOMALIA-1977).
FT   VARIANT     274    274       A -> E (IN STRAIN SOMALIA-1977).
FT   VARIANT     335    335       N -> D (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     339    339       P -> L (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;

  Query Match             20.2%;  Score 202.5;  DB 1;  Length 349;
  Best Local Similarity   33.8%;  Pred. No. 6.9e-10;
  Matches   52;  Conservative   18;  Mismatches   65;  Indels   19;  Gaps    7;

Qy      16 LLLLLNLFLPVI---------FAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIP 66
           :| |  |||  |         :  |      | | ||: :::|| :|| ||:    |
Db       4 VLYLYILFLSCIIINGRDAAPYTPPNG---KCKDTEYKRHNLCCLSCPPGTYASRLCD-S 59

Qy      67 HTQGQCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDP 125
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          |  ||  |  |||| ::| |  |  |:  |: :|     |: | :| |||  | ||
Db     60 KTNTQCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPG-YYCLL 118

Qy    126 KFPESCRPC---TKCPQGIPVLQECNSTANTVCS 156
          |    |: |   |||  |  |     |  : :||
Db    119 KGSSGCKACVSQTKCGIGYGVSGH-TSVGDVICS 151


RESULT 12
TR1A_BOVIN
ID   TR1A_BOVIN     STANDARD;      PRT;   471 AA.
AC   O19131;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98273505; PubMed=9613449;
RA   Lee E.-K., Kehrli M.E. Jr., Taylor M.J.;
RT   "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
RT   (TNF)-receptor I.";
RL   Vet. Immunol. Immunopathol. 61:379-385(1998).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U90937; AAB65143.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    471       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    471       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      340    360       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      372    457       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    194       BY SIMILARITY.
FT   DISULFID    185    190       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   471 AA;  51367 MW;  5243EF514DFE81C4 CRC64;

  Query Match             19.6%;  Score 196;  DB 1;  Length 471;
  Best Local Similarity   31.1%;  Pred. No. 3e-09;
  Matches   51;  Conservative   18;  Mismatches   63;  Indels   32;  Gaps    8;

Qy     18 LLLNLFLPVIFA----------MP-----ESYSFNCPDGEY---QSNDVCCKTCPSGTFV 59
          ||| | || : |          :|     |     || |:|   |:: :|| |  ||::
Db      9 LLLPLVLPALLADVYPAGVQGLVPHPGDLEKRESPCPQGKYNHPQNSTICCTKCHKGTYL 68

Qy     60 KAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKD--QNMVADCSATSDRKCEC- 116
             |  |     |  | |||:|  :| |  |  || |  :  |  :: |    |  | |
Db     69 YNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCSRCRDEMFQVEISPCVVDRDTVCGCR 128

Qy    117 --QIGLYYYDPKFPESCRPCTKCPQG---IPVLQECNSTANTVC 155
            |   |: :  |   |  |: || |   ||    |    :|:|
Db    129 KNQYREYWGETGF--RCLNCSLCPNGTVNIP----CQERQDTIC 166


RESULT 13
TNR6_RAT
ID   TNR6_RAT       STANDARD;      PRT;   324 AA.
AC   Q63199;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR PT1 OR FAS.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=94128114; PubMed=7507668;
RA   Kimura K., Yamamoto M., Wakatsuki T.;
RT   "A variant mRNA species encoding a truncated form of Fas antigen in
RT   the rat liver.";
RL   Biochem. Biophys. Res. Commun. 198:666-674(1994).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
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CC       both (By similarity).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC        AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC    -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC    -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC    ---------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    ---------------------------------------------------------------------
DR    EMBL; D26112; BAA05108.1; -.
DR    HSSP; P25445; 1DDF.
DR    InterPro; IPR000488; Death.
DR    InterPro; IPR001368; TNFR_c6.
DR    Pfam; PF00020; TNFR_c6; 3.
DR    Pfam; PF00531; death; 1.
DR    SMART; SM00005; DEATH; 1.
DR    SMART; SM00208; TNFR; 3.
DR    PROSITE; PS00652; TNFR_NGFR_1; 2.
DR    PROSITE; PS50050; TNFR_NGFR_2; 2.
DR    PROSITE; PS50017; DEATH_DOMAIN; 1.
KW    Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT    SIGNAL       1     21       BY SIMILARITY.
FT    CHAIN       22    324       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 6.
FT    DOMAIN      22    171       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM   172    188       POTENTIAL.
FT    DOMAIN     189    324       CYTOPLASMIC (POTENTIAL).
FT    REPEAT      43     79       TNFR-CYS 1.
FT    REPEAT      80    123       TNFR-CYS 2.
FT    REPEAT     124    163       TNFR-CYS 3.
FT    DOMAIN     219    303       DEATH.
FT    DISULFID    44     55       BY SIMILARITY.
FT    DISULFID    56     69       BY SIMILARITY.
FT    DISULFID    59     78       BY SIMILARITY.
FT    DISULFID    81     97       BY SIMILARITY.
FT    DISULFID   100    115       BY SIMILARITY.
FT    DISULFID   103    123       BY SIMILARITY.
FT    DISULFID   125    139       BY SIMILARITY.
FT    DISULFID   142    154       BY SIMILARITY.
FT    DISULFID   145    162       BY SIMILARITY.
FT    CARBOHYD    43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT    CARBOHYD   114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT    CARBOHYD   132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ    SEQUENCE   324 AA;  36835 MW;  D25D583C909D9D09 CRC64;

  Query Match             19.4%;  Score 194;  DB 1;  Length 324;
  Best Local Similarity   27.1%;  Pred. No. 3.2e-09;
  Matches   52;  Conservative   26;  Mismatches   74;  Indels   40;  Gaps    9;

Qy      17 LLLLNLFLPVIFAMPE--------------------SYSFNCPDGEYQSNDVCCKTCP 54
           :| :   ||:: | ||                          || :| ||    ||: |
Db       1 MLWIMAVLPLVLAGPELNVRMQGTDSIFEGLELKRSVRETDNNCSEGLYQVGPFCCQPCQ 60

Qy      55 SGTFVKAPCKIPHTQGQCEKCHPGT----FTGKDNGLHDCELCSTCDKDQNMVAD--CSA 108
            |      |    | |    ||| |    :| : :    |  |: ||:   :  :  |:
Db      61 PGERKVKDCT---TSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTR 117

Qy     109 TSDRKCECQIGLYYYDPKFPESCRPCTKCPQGI-PVLQECNSTANTVCSSSVSNPR-NWL 166
           | : || |:   :| :    : |  || |  |:  :|: |  |:|| |    || :  ||
Db     118 TQNTKCRCKEN-FYCNASLCDHCYHCTSC--GLEDILEPCTRTSNTKCKKQSSNYKLLWL 174

Qy     167 FLL----MLIVF 174
           :|    :| || .
Db     175 LILPGLAILFVF 186


RESULT 14
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TR1A_PIG
ID    TR1A_PIG       STANDARD;      PRT;   461 AA.
AC    P50555;
DT    01-OCT-1996 (Rel. 34, Created)
DT    01-OCT-1996 (Rel. 34, Last sequence update)
DT    15-JUN-2002 (Rel. 41, Last annotation update)
DE    Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE    (TNF-R1) (TNF-RI) (p55).
GN    TNFRSF1A OR TNFR1.
OS    Sus scrofa (Pig).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX    NCBI_TaxID=9823;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Kidney;
RX    MEDLINE=96011645; PubMed=7590278;
RA    Suter B., Pauli U.H.;
RT    "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT    receptor.";
RL    Gene 163:263-266(1995).
CC    -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC        TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC        caspase-8 to the activated receptor. The resulting death-inducing
CC        signaling complex (DISC) performs caspase-8 proteolytic activation
CC        which initiates the subsequent cascade of caspases (aspartate-
CC        specific cysteine proteases) mediating apoptosis (By similarity).
CC    -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC        HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC        PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC        WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC        PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC        TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC        ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC        NF-KAPPA B SIGNALING (BY SIMILARITY).
CC    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC    -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC    -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC    ---------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    ---------------------------------------------------------------------
DR    EMBL; U19994; AAC48499.1; -.
DR    HSSP; P19438; 1TNR.
DR    InterPro; IPR000488; Death.
DR    InterPro; IPR001368; TNFR_c6.
DR    Pfam; PF00020; TNFR_c6; 3.
DR    Pfam; PF00531; death; 1.
DR    ProDom; PD000771; TNFR_c6; 1.
DR    SMART; SM00005; DEATH; 1.
DR    SMART; SM00208; TNFR; 3.
DR    PROSITE; PS00652; TNFR_NGFR_1; 3.
DR    PROSITE; PS50050; TNFR_NGFR_2; 2.
DR    PROSITE; PS50017; DEATH_DOMAIN; 1.
KW    Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT    SIGNAL       1     21       POTENTIAL.
FT    CHAIN       22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 1A.
FT    DOMAIN      22    210       EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM   211    233       POTENTIAL.
FT    DOMAIN     234    461       CYTOPLASMIC (POTENTIAL).
FT    REPEAT      43     82       TNFR-CYS 1.
FT    REPEAT      83    125       TNFR-CYS 2.
FT    REPEAT     126    166       TNFR-CYS 3.
FT    REPEAT     167    195       TNFR-CYS 4.
FT    DOMAIN     340    350       N-SMASE ACTIVATION DOMAIN (NSD).
FT    DOMAIN     362    447       DEATH.
FT    DISULFID    44     58       BY SIMILARITY.
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FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    194       BY SIMILARITY.
FT   DISULFID    185    190       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50696 MW;  CD72361EC60C9D43 CRC64;

  Query Match           19.4%;  Score 193.5;  DB 1;  Length 461;
  Best Local Similarity  32.3%;  Pred. No. 4.7e-09;
  Matches   41;  Conservative   17;  Mismatches   58;  Indels   11;  Gaps    5;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   |:  :|| |  ||::   |  |     | :|  ||||  :| |  |  ||
Db      44 CPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCS 103

Qy      95 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
             |  : : |  : |:   |  | |   |   |: :  |   |  |: || |  |   |
Db     104 KCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLF--QCLNCSLCPNG-TVQLPCLE 160

Qy     150 TANTVCS 156
             :|:|:
Db     161 KQDTICN 167


RESULT 15
TNR6_HUMAN
ID   TNR6_HUMAN     STANDARD;      PRT;   335 AA.
AC   P25445; Q14293; Q14294; Q14295; Q14292; Q16652;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS OR FAS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91309137; PubMed=1713127;
RA   Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA   Sameshima M., Hase A., Seto Y., Nagata S.;
RT   "The polypeptide encoded by the cDNA for human cell surface antigen
RT   Fas can mediate apoptosis.";
RL   Cell 66:233-243(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
RP   321-335.
RX   MEDLINE=92268122; PubMed=1375228;
RA   Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA   Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA   Krammer P.H.;
RT   "Purification and molecular cloning of the APO-1 cell surface
RT   antigen, a member of the tumor necrosis factor/nerve growth factor
RT   receptor superfamily. Sequence identity with the Fas antigen.";
RL   J. Biol. Chem. 267:10709-10715(1992).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
RX   MEDLINE=95181785; PubMed=7533181;
RA   Cascino I., Fiucci G., Papoff G., Ruberti G.;
RT   "Three functional soluble forms of the human apoptosis-inducing Fas
RT   molecule are produced by alternative splicing.";
RL   J. Immunol. 154:2706-2713(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 5).
RC   TISSUE=Peripheral blood lymphocytes;
RA   Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RX   MEDLINE=96238926; PubMed=8648105;
RA   Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;
RT   "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants
RT   prevents cell death in vitro.";
RL   J. Immunol. 156:4622-4630(1996).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Urinary bladder;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   STRUCTURE BY NMR OF 218-335.
RX   MEDLINE=97122332; PubMed=8967952;
RA   Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT   "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL   Nature 384:638-641(1996).
RN   [8]
RP   VARIANT ALPS PRO-241.
RX   MEDLINE=95300225; PubMed=7540117;
RA   Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
RA   Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;
RT   "Dominant interfering Fas gene mutations impair apoptosis in a human
RT   autoimmune lymphoproliferative syndrome.";
RL   Cell 81:935-946(1995).
RN   [9]
RP   VARIANT ALPS TYR-260.
RX   MEDLINE=97066823; PubMed=8929361;
RA   Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
RT   "Fas gene mutations in the Canale-Smith syndrome, an inherited
RT   lymphoproliferative disorder associated with autoimmunity.";
RL   New Engl. J. Med. 335:1643-1649(1996).
RN   [10]
RP   VARIANTS ALPS TRP-121 AND CYS-232.
RX   MEDLINE=97180145; PubMed=9028321;
RA   Bettinardi A., Brugnoni D., Quiros-Roldan E., Malagoli A.,
RA   La Grutta S., Correra A., Notarangelo L.D.;
RT   "Missense mutations in the Fas gene resulting in autoimmune
RT   lymphoproliferative syndrome: a molecular and immunological
RT   analysis.";
RL   Blood 89:902-909(1997).
RN   [11]
RP   VARIANTS ALPS ASP-257 AND SER-310.
RX   MEDLINE=97180739; PubMed=9028957;
RA   Sneller M.C., Wang J., Dale J.K., Strober W., Middelton L.A., Choi Y.,
RA   Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
RA   Straus S.E.;
RT   "Clincial, immunologic, and genetic features of an autoimmune
RT   lymphoproliferative syndrome associated with abnormal lymphocyte
RT   apoptosis.";
RL   Blood 89:1341-1348(1997).
RN   [12]
RP   VARIANT ALPS ALA-28.
RX   MEDLINE=97463833; PubMed=9322534;
RA   Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
RA   Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
RA   Levrero M.;
RT   "Fas/Apo1 mutations and autoimmune lymphoproliferative syndrome in a
RT   patient with type 2 autoimmune hepatitis.";
RL   Gastroenterology 113:1384-1389(1997).
RN   [13]
RP   VARIANT ALPS VAL-260.
RX   MEDLINE=99038860; PubMed=9821419;
RA   Infante A.J., Britton H.A., DeNapoli T., Middelton L.A., Lenardo M.J.,
RA   Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;
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RT   "The clinical spectrum in a large kindred with autoimmune
RT   lymphoproliferative syndrome caused by a Fas mutation that impairs
RT   lymphocyte apoptosis.";
RL   J. Pediatr. 133:629-633(1998).
RN   [14]
RP   VARIANTS ALPS LYS-241 AND GLN-250.
RX   MEDLINE=99192346; PubMed=10090885;
RA   Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
RA   Dale J.K., Fleisher T.A., Middelton L.A., Sneller M.C., Lenardo M.J.,
RA   Straus S.E., Puck J.M.;
RT   "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
RT   influences penetrance.";
RL   Am. J. Hum. Genet. 64:1002-1014(1999).
RN   [15]
RP   VARIANT ALPS GLY-272.
RX   MEDLINE=99270228; PubMed=10340403;
RA   Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,
RA   Gahr M., Roesler J.;
RT   "Defective apoptosis due to a point mutation in the death domain of
RT   CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
RT   lymphoma, and Hodgkin's disease.";
RL   Exp. Hematol. 27:868-874(1999).
RN   [16]
RP   VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
RX   MEDLINE=99126461; PubMed=9927496;
RA   Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,
RA   Elkon K.B.;
RT   "The molecular basis for apoptotic defects in patients with CD95
RT   (Fas/Apo-1) mutations.";
RL   J. Clin. Invest. 103:355-363(1999).
RN   [17]
RP   VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
RP   VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
RX   MEDLINE=99005325; PubMed=9787134;
RA   Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,
RA   Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
RT   "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
RT   extranodal disease and autoimmunity.";
RL   Blood 92:3018-3024(1998).
RN   [18]
RP   VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
RX   MEDLINE=21311411; PubMed=11418480;
RA   Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
RA   Roesen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
RA   Fischer R.E., Jackson C.M., Lin A.Y., Baeumler C., Siegert E.,
RA   Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
RT   "The development of lymphomas in families with autoimmune
RT   lymphoproliferative syndrome with germline Fas mutations and
RT   defective lymphocyte apoptosis.";
RL   Blood 98:194-200(2001).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC       Secreted (isoforms 2 to 6).
CC   -!- ALTERNATIVE PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d,
CC       3/Del3/e, 4/b, 5/c and 6/TMDel/a; are produced by alternative
CC       splicing.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
CC       lymphoproliferative syndrome (ALPS), also known as Canale-Smith
CC       syndrome (CSS), a childhood syndrome involving hemolytic anemia
CC       and thrombocytopenia with massive lymphadenopathy and
CC       splenomegaly.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M67454; AAA63174.1; -.
DR   EMBL; X63717; CAA45250.1; -.
DR   EMBL; X89101; CAA61473.1; -.
DR   EMBL; Z47993; CAA88031.1; -.
DR   EMBL; Z47994; CAA88032.1; -.
DR   EMBL; Z47995; CAA88033.1; -.
DR   EMBL; Z70520; CAA94431.1; -.

  Query Match             18.9%;  Score 189.5;  DB 1;  Length 335;
  Best Local Similarity   30.9%;  Pred. No. 7.7e-09;
  Matches   42;  Conservative   19;  Mismatches   68;  Indels    7;  Gaps    5;

Qy      40 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 98
           :| :     | | || |      | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109

Qy      99 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             :  :  |: | : || |:   :: :    | | |||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     157 SSVSNPR-NWLFLLML 171
             |     || ||:|
Db     167 EEGSRSNLGWLCLLLL 182


Search completed: December 10, 2002, 15:06:15
Job time : 9.69136 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:03:51 ; Search time 28.7901 Seconds
(without alignments)
1259.609 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	288.5	28.8	438	13	Q9DFV0	Q9dfv0 brachydanio
2	250	25.0	357	13	Q9DF34	Q9df34 brachydanio
3	231	23.1	347	12	O57119	O57119 cowpox viru
4	226	22.6	360	12	O57118	O57118 cowpox viru
5	224.5	22.4	189	6	Q95185	Q95185 felis silve
6	222.5	22.2	446	6	Q95ND3	Q95nd3 felis silve
7	220.5	22.1	327	6	O97491	O97491 ovis aries
8	220	22.0	263	6	Q9XS60	Q9xs60 oryctolagus
9	220	22.0	320	6	Q9XS29	Q9xs29 oryctolagus
10	219	21.9	319	6	Q9TV79	Q9tv79 oryctolagus
11	217.5	21.8	351	12	O57121	O57121 cowpox viru
12	213.5	21.3	189	6	O97530	O97530 canis famil
13	213.5	21.3	349	12	O57305	O57305 cowpox viru
14	211.5	21.1	348	12	O57103	O57103 monkeypox v
15	211.5	21.1	348	12	O57108	O57108 monkeypox v
16	211.5	21.1	348	12	O57277	O57277 monkeypox v
17	211.5	21.1	349	12	O57101	O57101 monkeypox v
18	211.5	21.1	349	12	O57102	O57102 monkeypox v
19	211.5	21.1	349	12	O57291	O57291 monkeypox v
20	211.5	21.1	351	12	O73559	O73559 cowpox viru
21	209.5	20.9	326	12	O57120	O57120 cowpox viru
22	208.5	20.8	349	12	O57098	O57098 camelpox vi
23	208.5	20.8	349	12	O57099	O57099 monkeypox v
24	208.5	20.8	349	12	Q8UYA7	Q8uya7 camelpox vi
25	208.5	20.8	349	12	O57284	O57284 camelpox vi
26	207.5	20.8	326	12	O57122	O57122 cowpox viru
27	207.5	20.8	347	12	O57115	O57115 cowpox viru
28	207.5	20.8	349	12	O57109	O57109 variola vir
29	207.5	20.8	351	12	O57117	O57117 cowpox viru
30	206.5	20.6	355	12	Q85308	Q85308 cowpox viru
31	205.5	20.5	349	12	O57100	O57100 monkeypox v
32	204	20.4	348	12	O57112	O57112 variola vir
33	204	20.4	348	12	Q85407	Q85407 variola vir
34	203	20.3	350	12	O57123	O57123 cowpox viru
35	202.5	20.2	349	12	O57097	O57097 camelpox vi
36	202.5	20.2	349	12	O57110	O57110 variola vir
37	202.5	20.2	349	12	O57111	O57111 variola vir
38	202.5	20.2	349	12	Q89098	Q89098 variola vir
39	202.5	20.2	349	12	Q89118	Q89118 variola vir
40	196.5	19.7	320	12	O57079	O57079 cowpox viru
41	194	19.4	413	11	Q99MM1	Q99mm1 mus musculu
42	192.5	19.2	322	12	O72761	O72761 cowpox viru
43	190.5	19.1	331	6	Q9TSN4	Q9tsn4 macaca fasc
44	190.5	19.1	331	6	Q9BDN0	Q9bdn0 macaca neme
45	190.5	19.1	350	12	O57116	O57116 cowpox viru

ALIGNMENTS

RESULT 1
Q9DFV0
ID Q9DFV0 PRELIMINARY; PRT; 438 AA.
AC Q9DFV0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian TNF receptor.
GN TNFRSFA.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250042; AAG24365.1; -.
DR HSSP; O14763; 1D0G.
DR ZFIN; ZDB-GENE-010802-1; tnfrsfa.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;

Query Match 28.8%; Score 288.5; DB 13; Length 438;
Best Local Similarity 35.1%; Pred. No. 1.3e-23;

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  Matches   53;  Conservative   22;  Mismatches   59;  Indels   17;  Gaps    2;

Qy      42 EYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQN 101
           ||  |  ||| | :||:||  |   |  |:|  |  ||:     |:  |  || | :||
Db      49 EYPHNGFCCKNCEAGTYVKEKCTSGHVMGKCSPCEKGTYAEHPTGMEQCLQCSQCHRDQT 108

Qy     102 MVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC------ 155
           :||:|::||: ||:|: | :    :  | |: ||||      : |  |:|| |
Db     109 VVAECTSTSNTKCDCKFGTFCLPDEPCEVCKKCTKCKADEEEVSGCTPTSNTKCRRRPSY 168

Qy     156 -------SSSVSNPRNWLF----LLMLIVFC 175
                 | ||    :|    :|:|:| |
Db     169 PTEGPTEKPSASNSTGTIFVIVSILILLVIC 199


RESULT 2
Q9DF34
ID   Q9DF34      PRELIMINARY;      PRT;   357 AA.
AC   Q9DF34;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Death receptor.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT   "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
RT   receptor in transgenic zebrafish.";
RL   Nat. Cell Biol. 0:0-0(2000).
DR   EMBL; AF302789; AAG21396.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   357 AA;  40662 MW;  1652B4840D9EEDBA CRC64;

  Query Match           25.0%;  Score 250;  DB 13;  Length 357;
  Best Local Similarity   30.4%;  Pred. No. 1.9e-19;
  Matches   56;  Conservative   31;  Mismatches   71;  Indels   26;  Gaps    5;

Qy      15 LLLLLLNLFLPVIFAMPE--------------SYSFNCPDG-EYQSNDVCCKTCPSGTF 58
           |:|||||    || |                  |   :| :| ||   ::||  ||:||:
Db       7 LVLLLLN----VINAARSHGDLAWAHRSVKNRLSRDVSCREGLEYPHENICCLNCPAGTY 62

Qy      59 VKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQI 118
           ||  |     :| |  |   |:|  |:||  |  |  |  ||  :  |::| : :|:|:
Db      63 VKKACAAAAAEKGVCAPCEFDTYTEHDHGLLKCISCDKCRIDQETIEKCTSTQNTRCKCRN 122

Qy     119 GLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC----SSSVSNPRNWLFLLMLIVF 174
           | :    :  | |: |::| :     : | : :||||    |   |    :: :: |||
Db     123 GSFCLPDQACEVCKKCSRCKEDEETEKSCTAISNTVCRKRNSPGSSTSMTFIVIMPLIVL 182

Qy     175 --CI 176
             |:
Db     183 LACV 186


RESULT 3
O57119
ID   O57119      PRELIMINARY;      PRT;   347 AA.
AC   O57119;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH EP2-1975(ELEPHANT);
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90230; AAB94386.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   347 AA;  37971 MW;  A51B36A5619F48DA CRC64;

  Query Match           23.1%;  Score 231;  DB 12;  Length 347;
  Best Local Similarity   36.2%;  Pred. No. 2.4e-17;
  Matches   54;  Conservative   21;  Mismatches   66;  Indels    8;  Gaps    6;

Qy      14 FLLLLLLNLFLPVIFAMP-ESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQ 71
           ::|||||:  : :    | |  :  | | ||: : :|| :|| ||:    |    :|  |
Db       4 YILLLLLSCIIIINSETPHEPSNGKCKDNEYKHHHLCCLSCPPGTYASRLCDSKTNTNTQ 63

Qy      72 CEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPES 130
           |  |  |||| ::| |  |  |:  || :|      |: | :| |||  | ||   |
Db      64 CTSCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICECSPG-YYCLLKGSSG 122

Qy     131 CRPC---TKCPQGIPVLQECNSTANTVCS 156
           |: |   |||  |  |     || : :||
Db     123 CKACVSQTKCGMGYGVSGH-TSTGDVICS 150


RESULT 4
O57118
ID   O57118      PRELIMINARY;      PRT;   360 AA.
AC   O57118;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CPV58;
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90229; AAB94385.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
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SQ   SEQUENCE   360 AA;  39370 MW;  3628AD87E4709378 CRC64;

  Query Match             22.6%;  Score 226;  DB 12;  Length 360;
  Best Local Similarity   35.6%;  Pred. No. 8.7e-17;
  Matches   53;  Conservative   21;  Mismatches   67;  Indels    8;  Gaps    6;

Qy      14 FLLLLLLNLFLPVIFAMP-ESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQ 71
           ::||||||:  : :    | |  :  | | ||: : :|| :|| ||:    |    :|  |
Db       4 YILLLLLSCIIIIINSETPHEPSNGKCKDNEYKHHHLCCLSCPPGTYASRLCDSKTNTNTQ 63

Qy      72 CEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPES 130
           |  |  |||| ::| |  |  |:  || :|     |: | :| |||  | ||   |
Db      64 CTSCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICECSPG-YYCLLKGSSG 122

Qy     131 CRPC---TKCPQGIPVLQECNSTANTVCS 156
           |: |   |||  |  |      | : :||
Db     123 CKACVSQTKCGMGYGVSGH-TPTGDVICS 150


RESULT 5
Q95185
ID   Q95185      PRELIMINARY;      PRT;   189 AA.
AC   Q95185;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumour necrosis factor receptor p60 (Fragment).
GN   TNFR-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Duthie S., Nasir L., Eckersall P.D.;
RT   "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT   partial cds.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U72344; AAB95089.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  21420 MW;  F3FBE0CE809D7DBE CRC64;

  Query Match             22.4%;  Score 224.5;  DB 6;  Length 189;
  Best Local Similarity   34.4%;  Pred. No. 6.7e-17;
  Matches   53;  Conservative   20;  Mismatches   68;  Indels   13;  Gaps    6;

Qy      15 LLLLLLNLF-LPVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTCPSGTFVKAPCKI 65
           || ||: :: | |   :|      |  :  || |:|   | | :||  |  ||::   |:
Db      15 LLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDCEG 74

Qy      66 PHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKD--QNMVADCSATSDRKCECQIGLY-Y 122
           |     | :|  ||||  :| |  |  || | |:  |  :: |:   |  | |:   | |
Db      75 PGLDTDCRECENGTFTASENYLRQCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQYRY 134

Qy     123 YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           |  :    |  |: |  |  |   |  | ||||:
Db     135 YWSETHFQCLNCSLCLNG-TVQISCKETQNTVCT 167


RESULT 6
Q95ND3
ID   Q95ND3      PRELIMINARY;      PRT;   446 AA.
AC   Q95ND3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Tumor necrosis factor type I.
GN   TNFR I.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT   "Molecular cloning of feline tumor necrosis factor receptor type I
RT   (TNFR I ) and expression of TNFR I and TNFR II in various disease in
RT   cats.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB051103; BAB55455.1; -.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   446 AA;  49563 MW;  217BD331DD8A74AA CRC64;

  Query Match             22.2%;  Score 222.5;  DB 6;  Length 446;
  Best Local Similarity   34.4%;  Pred. No. 2.6e-16;
  Matches   53;  Conservative   19;  Mismatches   69;  Indels   13;  Gaps    6;

Qy      15 LLLLLLNLF-LPVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTCPSGTFVKAPCKI 65
           || ||: :: | |   :|      |  :  || |:|   | | :||  |  ||::   |
Db      15 LLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDCAG 74

Qy      66 PHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKD--QNMVADCSATSDRKCECQIGLY-Y 122
           |     | :|  ||||  :| |  |  || | |:  |  :: |:   |  | |:   | |
Db      75 PGLDTDCRECENGTFTASENYLRQCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQYRY 134

Qy     123 YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           |  :    |  |: |  |  |   |  | ||||:
Db     135 YWSETHFQCLNCSLCLNG-TVQISCKETQNTVCT 167


RESULT 7
O97491
ID   O97491      PRELIMINARY;      PRT;   327 AA.
AC   O97491;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Fas protein.
GN   FAS.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPHOCYTE;
RA   Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT   "Cloning of sheep fas antigen.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB011671; BAA37093.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
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DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   327 AA;  36928 MW;  5CFEE844B2BE387A CRC64;

  Query Match             22.1%;  Score 220.5;  DB 6;  Length 327;
  Best Local Similarity   30.6%;  Pred. No. 3.2e-16;
  Matches   44;  Conservative   28;  Mismatches   65;  Indels    7;  Gaps    5;

Qy      37 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT-FTGKDNGLHDCELCST 95
           :| :| |: :  ||: || |      ||      :|  |  |  :| | :    |  ||
Db      46 SCQEGLYREHLFCCQPCPPGKRKNGDCKRDGDMPECVLCSEGNEYTDKSHHSDKCIRCSV 105

Qy      96 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 153
           ||::  :  :  |: | : || |:   :: :    | | ||| |  ||  :::|  |:||
Db     106 CDEEHGLEVEHNCTRTQNTKCRCKSN-FFCNSSPCEHCNPCTTCEHGI--IEKCTPTSNT 162

Qy     154 VCSSSVSNPRN-WLFLLMLIVFCI 176
           |  | |:  : |  |::|::  |
Db     163 KCKGSRSHTNSLWALLILLLLILI 186


RESULT 8
Q9XS60
ID   Q9XS60      PRELIMINARY;      PRT;   263 AA.
AC   Q9XS60;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fas antigen spliced variant.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021297; BAA78429.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   263 AA;  30374 MW;  6D76782ADED1BFD7 CRC64;

  Query Match             22.0%;  Score 220;  DB 6;  Length 263;
  Best Local Similarity   30.2%;  Pred. No. 2.9e-16;
  Matches   54;  Conservative   23;  Mismatches   74;  Indels   28;  Gaps    7;

Qy      13 WFLLLLLLNLFLPVIFAMPESYSFNCPDGE----------YQSNDVCCKTCPSGTFVKAP 62
           | || |:|         :  | | :  | :          | | : ||: || ||  ||
Db       5 WVLLPLILT-------CIAGSLSTSINDCKIKNETQYSTGYLSGNFCCQLCPPGTKKKAD 57

Qy      63 CKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQNM--VADCSATSDRKCECQIG 119
           |     :  || |  |  :| | :    |  || || :  :    ||:   : || |:
Db      58 CTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEVETDCTTIQNTKCRCKSN 117

Qy     120 LYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRN-----WLFLLMLIV 173
           :    |  | | ||| |  ||  ::||  |:|| |    |  :     ||  ::|::
Db     118 FFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKGSTTGSKHHFLWLLCILLLI 173


RESULT 9
Q9XS29
ID   Q9XS29      PRELIMINARY;      PRT;   320 AA.
AC   Q9XS29;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-type FAS antigen.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021299; BAA78431.1; -.
DR   EMBL; AB021296; BAA78428.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   320 AA;  36102 MW;  DA235E243220FFB3 CRC64;

  Query Match             22.0%;  Score 220;  DB 6;  Length 320;
  Best Local Similarity   30.2%;  Pred. No. 3.6e-16;
  Matches   54;  Conservative   23;  Mismatches   74;  Indels   28;  Gaps    7;

Qy      13 WFLLLLLLNLFLPVIFAMPESYSFNCPDGE----------YQSNDVCCKTCPSGTFVKAP 62
           | || |:|         :  | | :  | :          | | : ||: || ||  ||
Db       5 WVLLPLILT-------CIAGSLSTSINDCKIKNETQYSTGYLSGNFCCQLCPPGTKKKAD 57

Qy      63 CKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQNM--VADCSATSDRKCECQIG 119
           |     :  || |  |  :| | :    |  || || :  :    ||:   : || |:
Db      58 CTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEVETDCTTIQNTKCRCKSN 117

Qy     120 LYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRN-----WLFLLMLIV 173
           :    |  | | ||| |  ||  ::||  |:|| |    |  :     ||  ::|::
Db     118 FFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKGSTTGSKHHFLWLLCILLLI 173


RESULT 10
Q9TV79
ID   Q9TV79      PRELIMINARY;      PRT;   319 AA.
AC   Q9TV79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   B-type Fas antigen.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021298; BAA78430.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   319 AA;  35961 MW;  06FA0033B1846591 CRC64;

  Query Match             21.9%;  Score 219;  DB 6;  Length 319;
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  Best Local Similarity   31.5%;  Pred. No. 4.6e-16;
  Matches   56;  Conservative   20;  Mismatches   74;  Indels   28;  Gaps    7;

Qy      13 WFLLLLLLNLFLPVIFAMPESYSFNCPDGE----------YQSNDVCCKTCPSGTFVKAP 62
           | || |:|         :  | | :  | :          | | : ||: || ||  ||
Db       5 WVLLPLILT-------CIAGSLSTSINDCKIKNETQYSTGYLSGNFCCQLCPPGTKKKAD 57

Qy      63 CKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQNM--VADCSATSDRKCECQIG 119
           |     :  || |  |  :| | :    |  || || :  :    ||:   : || |:
Db      58 CTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEVETDCTTIQNTKCRCKSN 117

Qy     120 LYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRN-----WLFLLMLI 172
           :    |  | | ||| |  ||  ::||  |:|| |    |   :     ||  |:||
Db     118 FFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKGSTTGSKHHLFWLSTLLLI 172


RESULT 11
O57121
ID   O57121      PRELIMINARY;      PRT;   351 AA.
AC   O57121;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH OPV89/4(CAT);
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90232; AAB94388.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   351 AA;  38394 MW;  6D0E4040C0EFEF78 CRC64;

  Query Match             21.8%;  Score 217.5;  DB 12;  Length 351;
  Best Local Similarity   36.3%;  Pred. No. 7.4e-16;
  Matches   53;  Conservative   16;  Mismatches   64;  Indels   13;  Gaps    6;

Qy      22 LFLPVIF------AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQCEK 74
           |||  |       |  |  :  | | ||: : :|| :|| ||:    |    :|  ||
Db      10 LFLSCIIINGRDVAPHEPSNGKCKDNEYKHHHLCCLSCPPGTYASRLCDSKTNTNTQCTS 69

Qy      75 CHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRP 133
           |  |||| ::| |  |  |:  || :|     |: | :| |||  | ||   |    |:
Db      70 CGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKA 128

Qy     134 C---TKCPQGIPVLQECNSTANTVCS 156
           |   |||  |  |     || : :||
Db     129 CVSQTKCGMGYGVSGH-TSTGDVICS 153


RESULT 12
O97530
ID   O97530      PRELIMINARY;      PRT;   189 AA.
AC   O97530;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor p60 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=21109092; PubMed=11182158;
RA   Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA   Bennett D.;
RT   "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL   Vet. Immunol. Immunopathol. 78:207-214(2001).
DR   EMBL; AF013955; AAD01516.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  21324 MW;  5D3AD6A5676BFE99 CRC64;

  Query Match             21.3%;  Score 213.5;  DB 6;  Length 189;
  Best Local Similarity   32.1%;  Pred. No. 1.1e-15;
  Matches   50;  Conservative   20;  Mismatches   69;  Indels   17;  Gaps    7;

Qy      15 LLLLLLNLF-LPVIFAMPE-----SYSFNCPDGEY---QSNDVCCKTCPSGTFVKAPCKI 65
           || ||| :: : |   :|         :  || |:|   | : :||  |  ||::   |
Db      15 LLALLLEIYPISVTALVPHPRNRVKRAILCPQGKYIHPQDDSICCTKCHKGTYLYNDCPG 74

Qy      66 PHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSDRKCEC---QIGL 120
           |     | :|  ||||  :| |  |  || | |: | |  : |:   |  | |   |
Db      75 PGLDTDCRECENGTFTASENHLRQCLSCSKCRKEMNQVEISPCTVYRDTVCGCRKNQYRF 134

Qy     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           |: :  |   |  |: |  |  |   |    ||:|:
Db     135 YWSETLF--QCNNCSLCLNG-TVQISCQEKQNTICT 167


RESULT 13
O57305
ID   O57305      PRELIMINARY;      PRT;   349 AA.
AC   O57305;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH OPV89/5(CAT), AND MUNICH OPV 91/1(CAT);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U90233; AAB94389.1; -.
DR   EMBL; U90228; AAB94384.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   349 AA;  38063 MW;  424EE08FDEDD04CF CRC64;

  Query Match             21.3%;  Score 213.5;  DB 12;  Length 349;
  Best Local Similarity   31.6%;  Pred. No. 2e-15;
  Matches   56;  Conservative   25;  Mismatches   71;  Indels   25;  Gaps    8;
```

```
Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Db       4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYRHHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           ||  |  |||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Db      64 QCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVKTRSCNTTHNRICDCAPG-YYCLLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
            |: |   |||          | |  |   |     : | ::|  |    ||  |::
Db     123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 14
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;

  Query Match             21.1%;  Score 211.5;  DB 12;  Length 348;
  Best Local Similarity   39.0%;  Pred. No. 3.4e-15;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy      38 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 96
           | | ||:| ::|| :|| ||:    |    |  ||  |   |||  :| |  |  |:  |
Db      32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy      97 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 153
           | :|     |: | :| |||  | ||   |    || |   |||  |  |     || :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy     154 VCS 156
           :||
Db     149 ICS 151


RESULT 15
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;

  Query Match             21.1%;  Score 211.5;  DB 12;  Length 348;
  Best Local Similarity   39.0%;  Pred. No. 3.4e-15;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy      38 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 96
           | | ||:| ::|| :|| ||:    |    |  ||  |   |||  :| |  |  |:  |
Db      32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy      97 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 153
           | :|     |: | :| |||  | ||   |    || |   |||  |  |     || :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy     154 VCS 156
           :||
Db     149 ICS 151


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Job time : 30.7901 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 14:56:26 ; Search time 29.2346 Seconds
(without alignments)
674.581 Million cell.updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	176	19	AAW80254	Amino acid sequenc
2	310	36.1	380	22	ABG09344	Novel human diagno
3	264.5	30.8	204	23	ABB81467	Murine TACH protei
4	209	24.4	461	11	AAR07450	Rat Tumour Necrosi
5	205	23.9	327	14	AAR41688	Murine Fas. Mus m
6	205	23.9	327	16	AAR78611	Murine Fas antigen
7	205	23.9	327	17	AAR92530	mFas sequence. Sy
8	205	23.9	327	20	AAW86241	Fas ligand (FasL)
9	205	23.9	327	21	AAB19344	Amino acid sequenc
10	204.5	23.8	285	18	AAW33359	TBP(20-190)/hCG-al
11	204.5	23.8	658	23	AAM49759	TNF-selectokine pr
12	200.5	23.4	139	22	AAB66977	Peptide: SEQ ID 12
13	200.5	23.4	154	21	AAY94711	Tumour necrosis fa
14	200.5	23.4	161	13	AAR27496	Native 30 kD TNF i
15	200.5	23.4	161	19	AAW59664	Human soluble tumo
16	200.5	23.4	161	19	AAW52267	Soluble tumour nec
17	200.5	23.4	161	20	AAW89233	Tumour necrosis in
18	200.5	23.4	161	22	AAB37676	Human 30 kDa TNF i
19	200.5	23.4	162	23	AAM48058	Human TNFR1 extrac
20	200.5	23.4	168	13	AAR24084	Truncated TNF-alph
21	200.5	23.4	199	13	AAR24080	Truncated TNF-alph
22	200.5	23.4	211	20	AAW89225	Tumour necrosis fa
23	200.5	23.4	256	18	AAW33357	TBP(20-161)/hCG-al
24	200.5	23.4	280	22	AAB66979	Tnfrl protein. Un
25	200.5	23.4	307	18	AAW33358	TBP(20-161)/hCG-be
26	200.5	23.4	309	16	AAR70108	TNF-R-GBPH fusion
27	200.5	23.4	311	20	AAW89229	Tumour necrosis fa
28	200.5	23.4	336	18	AAW33360	TBP(20-190)/hCG-be
29	200.5	23.4	349	22	AAB50523	Human tumour necro
30	200.5	23.4	366	20	AAW89228	Tumour necrosis fa
31	200.5	23.4	371	11	AAR07449	Tumour Necrosis Fa
32	200.5	23.4	397	20	AAW89227	Tumour necrosis fa
33	200.5	23.4	417	20	AAW89226	Tumour necrosis fa
34	200.5	23.4	420	20	AAW89224	Tumour necrosis fa
35	200.5	23.4	451	16	AAR70107	TNF-R-GBP 130 fusi
36	200.5	23.4	455	11	AAR07451	Human Tumour Necro
37	200.5	23.4	455	12	AAR10986	30kD TNF inhibitor
38	200.5	23.4	455	12	AAR11082	Human 55kD TNF-bin
39	200.5	23.4	455	13	AAR20787	TNF-alpha binding
40	200.5	23.4	455	13	AAR24000	TNF-alpha 55kD rec
41	200.5	23.4	455	14	AAR42059	Lambda derived TNF
42	200.5	23.4	455	16	AAR75084	p55 TNF-R. Homo s
43	200.5	23.4	455	20	AAY30934	Human tumour necro
44	200.5	23.4	455	21	AAB36266	Human tumour necro
45	200.5	23.4	455	21	AAB37800	Human tumour necro

ALIGNMENTS

RESULT 1
AAW80254
ID AAW80254 standard; Protein; 176 AA.
XX
AC AAW80254;
XX
DT 28-JAN-1999 (first entry)
XX
DE Amino acid sequence of protein 7F4.
XX
KW Protein 7F4; differentiation; osteoblast cell; bone growth;
KW bone sarcoma.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..176
FT /note= "mature protein"
XX
PN WO9843998-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1998; 98WO-JP01511.
XX
PR 01-APR-1997; 97JP-0099653.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Kimura N, Toyoshima T;
XX

DR WPI; 1998-568275/48.
DR N-PSDB; AAV68046.
XX
PT Receptor protein inducing differentiation in osteoblast cells - has
PT extracellular region only and can be used for screening substances
PT for treatment of bone growth disorders
XX
PS Claim 1; Pages 29-31; 51pp; Japanese.
XX
CC The present sequence represents a protein designated 7F4. This protein
CC is capable of inducing differentiation in osteoblast cells. The
CC protein may be used to screen compounds for the ability to bind to
CC it, for use as ligands, agonists or antagonists and inhibiting or
CC otherwise altering its differentiation inducing activity. Compounds
CC so identified, as well as the protein itself, DNA encoding it, and
CC antibodies to it, may be used in the treatment of diseases of bone
CC growth and osteoblast differentiation, such as bone sarcomas.
XX
SQ Sequence 176 AA;

Query Match 100.0%; Score 858; DB 19; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.6e-66;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 88

Qy      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 148

Qy     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
           ||||||||||||||||||||||||||||
Db     149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176
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RESULT 2
ABG09344
ID ABG09344 standard; Protein; 380 AA.
XX
AC ABG09344;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9335.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS73531.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 39703; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 380 AA;

Query Match 36.1%; Score 310; DB 22; Length 380;
Best Local Similarity 77.1%; Pred. No. 8e-19;
Matches 54; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

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Qy       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
           || | :|| || ||| | ||||| | :||||||||:||||||||||||||||| ||| |
Db     103 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD 162

Qy      61 DCELCSTCDK 70
              | |||||||
Db     163 ACILCSTCDK 172
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RESULT 3
ABB81467
ID ABB81467 standard; Protein; 204 AA.
XX
AC ABB81467;
XX
DT 29-AUG-2002 (first entry)
XX
DE Murine TACH protein SEQ ID NO:2.
XX
KW TACH; tumour necrosis factor receptor family; TNF receptor; cancer;
KW inflammatory; immunoregulatory; cytostatic; antiinflammatory;
KW gene therapy.
XX
OS Mus sp.
XX
PN WO200228900-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30993.
XX
PR 04-OCT-2000; 2000US-237791P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOX-) APOXIS BIOSCIENCES LTD.
XX
PI Zheng T, Tschopp J, Schneider P;
XX
DR WPI; 2002-507878/54.
DR N-PSDB; ABN89334.
XX
PT Novel isolated tumor necrosis factor receptor family member nucleic
PT acid, termed TACH, useful for diagnosing, treating, preventing or

```
PT   delaying cancer, inflammatory or immunoregulatory condition -
XX
PS   Claim 3; Fig 1; 87pp; English.
XX
CC   The present invention describes an isolated tumour necrosis factor (TNF)
CC   receptor family member, designated TACH (I). (I) has cytostatic and
CC   antiinflammatory activities, and can be used in gene therapy. (I) can
CC   be used for diagnosing, treating, preventing or delaying cancer,
CC   inflammatory or immunoregulatory conditions. (I) is also useful for
CC   modulating the activity of cytokines, in screening assays, detection
CC   assays (e.g. chromosomal mapping, tissue typing, forensic biology),
CC   predictive medicine (e.g. diagnostic assays, prognostic assays,
CC   monitoring clinical trials and pharmacogenomics), and in methods of
CC   treatment (e.g. therapeutic and prophylactic). The present sequence
CC   represents murine TACH from the present invention.
XX
SQ   Sequence   204 AA;

  Query Match             30.8%;  Score 264.5;  DB 23;  Length 204;
  Best Local Similarity   37.6%;  Pred. No. 3.4e-15;
  Matches   47;  Conservative   21;  Mismatches   56;  Indels    1;  Gaps    1;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCD 69
           |  ||::  ::||  | :||::: ||:  | : :|  |    |    |   :|  || |
Db      27 CKIGEFKHENLCCLQCSAGTYLRNPCQENHNKSECAPCDSEHFIDHKNRESECFPCSVCR 86

Qy      70 KDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSS 129
             ||  || || |:|| |:|: | |       | |  |: || |  |:::||:| :|||
Db      87 DDQEEVAKCSRTADRVCQCKQGTYCDSENCLERCHTCSSCPDG-RVVRKCNATMDTVCDK 145

Qy     130 SVSNP 134
           | | |
Db     146 FDSEP 150


RESULT 4
AAR07450
ID   AAR07450 standard; protein; 461 AA.
XX
AC   AAR07450;
XX
DT   29-JAN-1991  (first entry)
XX
DE   Rat Tumour Necrosis Factor-Receptor from raTNF-R8 cDNA.
XX
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   raTNF-R8.
XX
OS   Rat rattus.
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;   90EP-0106624.
XX
PR   21-JUN-1989;   89DE-3920282.
PR   21-APR-1989;   89DE-3913101.
XX
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
XX
PI   Hauptmann R,  Himmler A,  Maurer-Fogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
DR   N-PSDB; AAQ06284.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
XX
PS   Disclosure; Fig 8(1-2); 51pp; German.
XX
CC   A rat brain cDNA analogue of the HS913T cDNA library from rat
CC   glioma cell line C6 (ATCC CCL107) is prepared in lambda-gt11.
CC   The isolated clone raTNF-R8 is used as probe to isolated the entire
CC   human TNF receptor, as represented in AAQ06285.
CC   See also AAQ06282-Q06285.
XX
SQ   Sequence   461 AA;

  Query Match             24.4%;  Score 209;  DB 11;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 4.8e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  :: | |  |  | |   |   |  :  |   |  |: |  |  |  |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN----------WL 138
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148  .
           | :|   ||
Db     221 GLCLLFFICI 230


RESULT 5
AAR41688
ID   AAR41688 standard; Protein; 327 AA.
XX
AC   AAR41688;
XX
DT   19-APR-1994  (first entry)
XX
DE   Murine Fas.
XX
KW   Murine; Fas; human; macrophage; cell strain; BAM3.
XX
OS   Mus musculus.
XX
PN   JP05219959-A.
XX
PD   31-AUG-1993.
XX
PF   14-FEB-1992;   92JP-0028090.
XX
PR   14-FEB-1992;   92JP-0028090.
XX
PA   (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
XX
DR   WPI; 1993-308326/39.
DR   N-PSDB; AAQ48008.
XX
PT   DNA hybridising with sequence coding for human FAS protein - is
PT   prepd. from e.g. BAM3 cell of mouse macrophage cell
XX
PS   Claim 1; Page 6-7; 8pp; Japanese.
XX
CC   This sequence represents the murine Fas protein.  The cDNA encoding
CC   this sequence hybridises with the human Fas gene and was isolated
CC   from the mouse macrophage cell strain BAM3.  This sequence may be
CC   used for the production of large amounts of murine Fas.
XX
SQ   Sequence   327 AA;

  Query Match             23.9%;  Score 205;  DB 14;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 7.4e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102
```

```
Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
            |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 6
AAR78611
ID   AAR78611 standard; Protein; 327 AA.
XX
AC   AAR78611;
XX
DT   19-FEB-1996  (first entry)
XX
DE   Murine Fas antigen extracellular region.
XX
KW   Murine Fas antigen; extracellular region; soluble membrane protein;
KW   antibody production; diseases; treatment; prevention.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= sig_peptide
FT   Peptide         22..327
FT                   /label= mat_peptide
XX
PN   JP07115988-A.
XX
PD   09-MAY-1995.
XX
PF   26-OCT-1993;   93JP-0267644.
XX
PR   26-OCT-1993;   93JP-0267644.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 1995-202847/27.
DR   N-PSDB; AAQ95302.
XX
PT   Preparation of soluble membrane proteins - for their use in antibody
PT   production for the treatment and prevention of related diseases
XX
PS   Example 2; Pages 32-33; 51pp; Japanese.
XX
CC   AAQ95302 encodes AAR78611 the murine Fas antigen extracellular region.
CC   The cDNA was used in the construction of an expression vector for
CC   the prodn. of recombinant soluble membrane proteins. The proteins
CC   can be used in antibody prodn. for the treatment and prevention of
CC   related diseases.
XX
SQ   Sequence   327 AA;

  Query Match             23.9%;  Score 205;  DB 16;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 7.4e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |       ||:       |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
            |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180
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RESULT 7
AAR92530
ID   AAR92530 standard; Protein; 327 AA.
XX
AC   AAR92530;
XX
DT   06-SEP-1996  (first entry)
XX
DE   mFas sequence.
XX
KW   Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
KW   rheumatoid arthritis; serum; systemic lupus erythematosus.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /note= "signal peptide"
FT   Protein         22..327
FT                   /note= "mature Fas"
FT   Misc-difference 24
FT                   /note= "encoded by AGT"
XX
PN   WO9601277-A1.
XX
PD   18-JAN-1996.
XX
PF   03-MAR-1995;   95WO-JP00349.
XX
PR   14-FEB-1995;   95JP-0025637.
PR   06-JUL-1994;   94JP-0154706.
XX
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Hachiya T,  Noguchi J,  Yonehara S;
XX
DR   WPI; 1996-087635/09.
DR   N-PSDB; AAT16305.
XX
PT   Immunoassay method for soluble Fas antigen in body fluids - for
PT   diagnosis of auto:immune diseases such as rheumatoid arthritis and
PT   systemic lupus erythematosus
XX
PS   Example 9; Page 80-82; 124pp; Japanese.
XX
CC   This sequence represents the mFas antigen used for the mFas.EXT,
CC   contained within the plasmid pMEl8S.  The soluble Fas antigen is included
CC   in the immunoassay kit of the invention.  The kit is for the assay of
CC   soluble Fas antigen and contains an immobilised anti-soluble Fas
CC   monoclonal antibody, as well as the standard soluble Fas antigen
CC   represented by this sequence.  The assay is simple and has high accuracy,
CC   high sensitivity, and is capable of assaying a number of different
CC   specimens at the same time.  The immunoassay is used on biological
CC   samples (such as serum) and is useful for diagnosis of autoimmune
CC   diseases such as rheumatoid arthritis or systemic lupus erythematosus
CC   (SLE).
XX
SQ   Sequence   327 AA;

  Query Match             23.9%;  Score 205;  DB 17;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 7.4e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |       ||:       |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159
```

```
Qy    126 VCSSSVSNPRNWLFLLMLIVFCI 148
          |     :||| |:|| ::|  |
Db    160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 8
AAW86241
ID   AAW86241 standard; Protein; 327 AA.
XX
AC   AAW86241;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Fas ligand (FasL) protein.
XX
KW   Fas ligand; FasL; FAs receptor; tumour; non-tumourigenic; T cell;
KW   rhabdomyosarcoma; killing; myoblast cell; immune provocation;
KW   neutrophil; detection.
XX
OS   Mus sp.
XX
PN   WO9846242-A1.
XX
PD   22-OCT-1998.
XX
PF   10-APR-1998;   98WO-US07235.
XX
PR   11-APR-1997;   97US-0041880.
XX
PA   (STRD ) UNIV STANFORD.
XX
PI   Blau HM,  Hofmann A;
XX
DR   WPI; 1999-009332/01.
DR   N-PSDB; AAV71961.
XX
PT   Killing tumour cells which express the Fas receptor - by
PT   administering non-tumourigenic cells that express the Fas ligand to
PT   kill the tumour cells, e.g. rhabdomyosarcoma cells
XX
PS   Examples; Pages 23-25; 42pp; English.
XX
CC   This represents a Fas ligand (FasL) protein. This can be used in the
CC   method of the invention of killing of tumour cells which express the
CC   Fas receptor. The method comprises administering non-tumourigenic cells
CC   that express the FasL to kill the tumour cells. Rhabdomyosarcoma cells
CC   which express the Fas receptor can also be killed by administering
CC   myoblast cells that express the FasL. The methods can be used for the
CC   destruction of Fas receptor expressing tumour cells. They also provide a
CC   general immune provocation that stimulates the clearance of the tumour
CC   cells involving the infiltration of neutrophils into the area of
CC   administration of FasL-expressing cells and also the infiltration of
CC   T cells. The methods can also be used for the detection of the Fas
CC   receptor on cells.
XX
SQ   Sequence   327 AA;

  Query Match           23.9%;  Score 205;  DB 20;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 7.4e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy      9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
          || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db     43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy     68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
          ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db    103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy    126 VCSSSVSNPRNWLFLLMLIVFCI 148
          |     :||| |:|| ::|  |
Db    160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 9
AAB19344
ID   AAB19344 standard; Protein; 327 AA.
XX
AC   AAB19344;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Amino acid sequence of a murine Fas (Apo-1) protein.
XX
KW   Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
KW   Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW   autoimmune disease; inflammatory disease; lymphoma.
XX
OS   Mus musculus.
XX
PN   WO200061150-A1.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09540.
XX
PR   12-APR-1999;   99US-0290640.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dean NM,  Marcusson EG;
XX
DR   WPI; 2000-628395/60.
DR   N-PSDB; AAC61859.
XX
PT   Antisense oligonucleotides for treating hepatitis and colon, liver or
PT   lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT   1 (Fap-1) expression  -
XX
PS   Example 5; Page 108-109; 116pp; English.
XX
CC   The present sequence represents murine Fas (Apo-1). The specification
CC   describes antisense compounds which are targeted to the 5'-untranslated
CC   region, translational start site, translational termination region
CC   or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC   ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC   phosphatase). The antisense compounds are used to inhibit the
CC   expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC   to treat autoimmune or inflammatory diseases such as hepatitis. They
CC   can also be used to treat cancer, especially colon, liver or lung
CC   cancer or lymphoma.
XX
SQ   Sequence   327 AA;

  Query Match           23.9%;  Score 205;  DB 21;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 7.4e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy      9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
          || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db     43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy     68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
          ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db    103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy    126 VCSSSVSNPRNWLFLLMLIVFCI 148
          |     :||| |:|| ::|  |
Db    160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 10
AAW33359
ID   AAW33359 standard; Protein; 285 AA.
XX
AC   AAW33359;
```

```
XX
DT   19-MAR-1998  (first entry)
XX
DE   TBP(20-190)/hCG-alpha fusion protein.
XX
KW   Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
KW   alpha subunit; hCG-alpha.
XX
OS   Homo sapiens.
XX
PN   WO9730161-A1.
XX
PD   21-AUG-1997.
XX
PF   20-FEB-1997;   97WO-US02315.
XX
PR   20-FEB-1996;   96US-0011936.
XX
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI   Campbell RK,  Chappel SC,  Jameson BA;
XX
DR   WPI; 1997-425036/39.
DR   N-PSDB; AAT94021.
XX
PT   Hybrid dimeric protein comprising two co-expressed units - each
PT   based on receptor or ligand and a subunit of a heterodimeric
PT   hormone, especially FSH, for inducing follicular maturation
XX
PS   Example; Pages 37-38; 60pp; English.
XX
CC   A novel fusion protein comprises 2 dimer forming co-expressed amino
CC   acid sequences, each consisting of a homodimeric or heterodimeric
CC   receptor chain or ligand, with ligand-receptor binding activity,
CC   bound directly or via a peptide linker to a subunit of a
CC   heterodimeric protein hormone capable of forming a heterodimer with
CC   the hormone's other subunits. The fusion protein, e.g. the
CC   thrombopoietin (TPO)/human chorionic gonadotrophin-alpha subunit
CC   (hCG-alpha) fusion protein denoted by the present sequence,
CC   significantly increases the biological activity of the hormone
CC   component, reducing the requirement for hormone itself and the
CC   number of injections needed.
XX
SQ   Sequence   285 AA;

  Query Match             23.8%;  Score 204.5;  DB 18;  Length 285;
  Best Local Similarity   34.4%;  Pred. No. 7e-10;
  Matches   43;  Conservative   15;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db      26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  || |  |  |   |
Db      86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNG-TVHLSCQEKQ 144

Qy     124 NTVCS 128
           ||||:
Db     145 NTVCT 149


RESULT 11
AAM49759
ID   AAM49759 standard; Protein; 658 AA.
XX
AC   AAM49759;
XX
DT   05-JUL-2002  (first entry)
XX
DE   TNF-selectokine prodrug W24.
XX
KW   Prodrug; W24; TNF; tumour necrosis factor; selectokine; chimeric;
KW   cytostatic; immunomodulatory; antiangiogenic; apoptosis inducer;
KW   gene therapy; scFv antibody OS4; fibroblast activation protein;
KW   solid tumour; angiogenesis; treatment; infection; metabolic disease.
XX
OS   Homo sapiens - Chimeric.
OS   Gallus sp - Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= leader_peptide
FT   Region          20..285
FT                   /note= "scFv antibody OS4 specific for human
FT                         fibroblast activiation protein (FAP)"
FT   Protein         20..658
FT                   /label= mature_W24
FT   Domain          286..315
FT                   /note= "chicken tenascin trimerising domain"
FT   Region          316..321
FT                   /note= "linker region"
FT   Region          322..486
FT                   /note= "mutated form of human TNF precursor protein
FT                         (26 kDa membrane form) with a deletion in the
FT                         N-terminal region of the first 56 amino acids
FT                         and from aa78-89 (TNFdeltal-56,78-89), i.e. a
FT                         deletion in the cytoplasmic domain, the
FT                         transmembrane domain and the TACE cleavage
FT                         site"
FT   Region          487..512
FT                   /note= "linker region with protease cleavage site"
FT   Region          513..639
FT                   /note= "human TNFR1 fragment containing extracellular
FT                          domains 1-3"
FT   Region          640..652
FT                   /note= "Myc-tag"
FT   Region          653..658
FT                   /note= "His-tag"
XX
PN   WO200222833-A1.
XX
PD   21-MAR-2002.
XX
PF   17-SEP-2001; 2001WO-EP10730.
XX
PR   15-SEP-2000; 2000DE-1045592.
XX
PA   (UYST-) UNIV STUTTGART.
PA   (PFIZ/) PFIZENMAIER K.
XX
PI   Pfizenmaier K,  Wuest T,  Moosmayer D,  Grell M,  Scheurich P;
XX
DR   WPI; 2002-362351/39.
DR   N-PSDB; ABA99913.
XX
PT   New polypeptide prodrug, useful e.g. for treating tumors, contains
PT   targeting region, active agent and attached inhibitor that is
PT   proteolytically cleaved in target cells -
XX
PS   Example 3; Fig 1; 52pp; German.
XX
CC   This invention describes a novel polypeptide (I) comprising, in the N
CC   to C direction, a region (R1) that recognises selectively a specific
CC   macromolecule on a cell surface and/or a component of the extracellular
CC   matrix, peptide linker, a region (R2) with biological activity for a
CC   specific target molecule, a region (R3) that has a processing site and a
CC   region (R4) that inhibits the activity of R2, by intramolecular bonding
CC   and/or interaction. The products of the invention have cytostatic,
CC   immunomodulatory and antiangiogenic activity, induce apoptosis and can be
CC   used for gene therapy. Kym-1 cells (20000) were incubated with the
CC   prodrug W24, containing, essentially, the single-chain Fv antibody OS4,
CC   specific for human fibroblast activation protein, trimerization linker,
CC   mutant form of the tumour necrosis factor (TNF) precursor protein, a
CC   region with a proteolytic cleavage site, and human TNF receptor-1
CC   fragment, and with trypsin (activator) for 5 minutes. After 16 hours,
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CC   cell viability was determined by MTT staining. Activated W24 had LD50
CC   about 0.5 ng/ml, comparable with that for wild-type TNF and 4000 times
CC   higher than for uncleaved W24. (I), also nucleic acids encoding them and
CC   related vectors, are useful particularly for treating solid tumours
CC   and/or pathological angiogenesis, also generally for treating infections
CC   and metabolic diseases. (I) are prodrug forms of R2 that have
CC   unacceptable toxicity when administered systemically (specifically tumour
CC   necrosis factor) and allow these compounds to be administered safely with
CC   retention of, or even increase in, therapeutic activity. R2 is released
CC   only in target tissue, resulting in a high local concentration, and
CC   activity is potentiated by co-activation of receptors. This sequence
CC   represents the TNF-selectokine W24 prodrug described in the disclosure of
CC   the invention.
XX
SQ   Sequence   658 AA;

  Query Match             23.8%;  Score 204.5;  DB 23;  Length 658;
  Best Local Similarity   33.9%;  Pred. No. 1.7e-09;
  Matches   43;  Conservative   16;  Mismatches   61;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db     516 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 575

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
           | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db     576 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 634

Qy     124 NTVCSSS 130
           ||||: |
Db     635 NTVCTGS 641


RESULT 12
AAB66977
ID   AAB66977 standard; Protein; 139 AA.
XX
AC   AAB66977;
XX
DT   19-APR-2001  (first entry)
XX
DE   Peptide: SEQ ID 126.
XX
KW   Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW   multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW   systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW   acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
KW   coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW   endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
KW   ischaemia; Parkinson's disease.
XX
OS   Unidentified.
XX
PN   WO200103719-A2.
XX
PD   18-JAN-2001.
XX
PF   07-JUL-2000; 2000WO-US18667.
XX
PR   09-JUL-1999;   99US-0350670.
PR   09-DEC-1999;   99US-0457647.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Lacey DL,  Calzone FJ,  Chang M,  Senaldi G;
XX
DR   WPI; 2001-103031/11.
XX
PT   Treating conditions leading to bone loss such as rheumatoid arthritis,
PT   multiple sclerosis and asthma, comprises administering an
PT   osteoprotegerin protein in conjunction with e.g. inhibitors of
PT   interleukin and tumor necrosis factor alpha  -
XX
PS   Disclosure; Pages 292-293; 316pp; English.
XX
CC   The present invention relates to a method for treating conditions leading
CC   to bone loss. The method comprises administering a purified and isolated
CC   osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
CC   in conjunction with other substances such as tumour necrosis factor-alpha
CC   (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC   modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
CC   activating factor (PAF) antagonists. The method is useful for treating
CC   conditions leading to bone loss such as rheumatoid arthritis, multiple
CC   sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC   useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC   graft-versus-host disease (GvHD). Other diseases that can be treated
CC   include acute pancreatitis, Alzheimer's disease, anorexia,
CC   atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC   cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC   inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC   psoriasis and septic shock.
XX
SQ   Sequence   139 AA;

  Query Match             23.4%;  Score 200.5;  DB 22;  Length 139;
  Best Local Similarity   33.6%;  Pred. No. 7.3e-10;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db      1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
           | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 119

Qy     124 NTVCS 128
           ||||:
Db     120 NTVCT 124

-
RESULT 13
AAY94711
ID   AAY94711 standard; Protein; 154 AA.
XX
AC   AAY94711;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Tumour necrosis factor receptor (TNFR) domain of TNFR-1.
XX
KW   Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW   chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW   immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW   severely combined immunodeficiency; apoptosis inhibition;
KW   Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS   Homo sapiens.
XX
PN   WO200056405-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07521.
XX
PR   22-MAR-1999;   99US-0125683.
PR   26-MAR-1999;   99US-0126522.
PR   20-MAY-1999;   99US-0135169.
PR   06-AUG-1999;   99US-0147383.
XX
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (GENT/) GENTZ R L.
XX
PI   Ni J,  Rosen CA,  Gentz RL;
XX
```

```
DR   WPI; 2000-594519/56.
XX
PT   Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT   and its two splice variants, useful for treating arthritis or
PT   inflammation, cancer (such as follicular lymphomas) and
PT   immunodeficiency disorders -
XX
PS   Disclosure; Fig 16; 373pp; English.
XX
CC   This invention relates to an isolated nucleic acid molecule encoding a
CC   human tumour necrosis factor(TNF)-receptor related protein TR2. Included
CC   in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC   The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
CC   member of the TNFR superfamily. The invention includes a method for the
CC   treatment of arthritis or inflammation using an antibody directed against
CC   a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC   antibodies exhibit cytostatic, dermatological, antianaemic,
CC   immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
CC   antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC   cerebroprotective activity. The methods are useful for treating arthritis
CC   or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
CC   mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
CC   immunodeficiency or for enhancing an in vivo leukocyte response to an
CC   antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC   preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC   dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC   inflammatory myopathies) and immunodeficiency disorders (such as severely
CC   combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC   disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
CC   TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
CC   antagonists are useful for treating or preventing autoimmune diseases and
CC   inhibit the growth, progression and/or metastasis of cancers. They are
CC   also used to activate, differentiate or proliferate cancerous cells or
CC   tissues, and can be used to treat diseases associated with increased cell
CC   survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
CC   Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
CC   as sources for generating antibodies, as molecular weight markers.
CC   This sequence represents the tumour necrosis factor receptor (TNFR)
CC   domain of the human TNFR-1 protein. The sequence was used in the
CC   characterisation of the TR2 receptor protein of the invention.
XX
SQ   Sequence   154 AA;

  Query Match             23.4%;  Score 200.5;  DB 21;  Length 154;
  Best Local Similarity   33.6%;  Pred. No. 8.1e-10;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::  |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
             | |:   |  : |:   |  | |:   | :|  :    |  |:| |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 14
AAR27496
ID   AAR27496 standard; protein; 161 AA.
XX
AC   AAR27496;
XX
DT   09-MAR-1993  (first entry)
XX
DE   Native 30 kD TNF inhibitor.
XX
KW   Tumour necrosis factor; ethylene glycol; pharmokinetic;
KW   adult respiratory distress syndrome; rheumatoid arthritis;
KW   septic shock; pulmonary fibrosis; spacer.
XX
OS   Homo sapiens.
XX
PN   WO9216221-A.
XX
PD   01-OCT-1992.
XX
PF   13-MAR-1992;   92WO-US02122.
XX
PR   15-MAR-1991;   91US-0669862.
PR   17-JAN-1992;   92US-0822296.
XX
PA   (SYND ) SYNERGEN INC.
XX
PI   Armes LG,  Brewer MT,  Evans RJ,  Kohno T,  Thompson RC;
XX
DR   WPI; 1992-348933/42.
XX
PT   New ethylene glycolated polypeptide(s) with improved
PT   pharmacokinetic properties - for treating e.g. TNF and IL-1
PT   mediated diseases, e.g. adult respiratory distress syndrome,
PT   rheumatoid arthritis, septic shock etc.
XX
PS   Claim 54; Fig 2; 100pp; English.
XX
CC   The sequence shows a native 30 kD TNF inhibitor which may be
CC   modified to contain at least one non-native cysteine residue, pref.
CC   at positions 1, 14, 105, 111 and/or 165.  The non-native cysteine is
CC   joined to a non-peptidic polymer, pref. monomethoxy PEG via
CC   thio-ether bonds.  Two such TNF inhibitor mols. may be linked via
CC   this non-peptidic spacer.  The modified polypeptides show improved
CC   pharmokinetic properties, i.e. increased mol. wt. hence reduced
CC   clearance rate following s.c. or systemic administration, increased
CC   sol. of native TNF inhibitors, and reduced antigenicity.  The
CC   polypeptides may be used for treatment of TNF mediated diseases such
CC   as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
CC   arthritis,inflammatory bowel disease and septic shock.  The same
CC   method may be applied to the interleukin-1 receptor antagonist
CC   IL-1ra.            See also AAR27495.
XX
SQ   Sequence   161 AA;

  Query Match             23.4%;  Score 200.5;  DB 13;  Length 161;
  Best Local Similarity   33.6%;  Pred. No. 8.5e-10;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::  |  |     | :|  |:||  :| |  |  ||
Db       4 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 63

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
             | |:   |  : |:   |  | |:   | :|  :    |  |:| |  |  |   |
Db      64 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 122

Qy     124 NTVCS 128
           ||||:
Db     123 NTVCT 127


RESULT 15
AAW59664
ID   AAW59664 standard; Protein; 161 AA.
XX
AC   AAW59664;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Human soluble tumour necrosis factor receptor type I.
XX
KW   Human; tumour necrosis factor; TNF; TNF receptor type I;
KW   inflammatory disease; leukaemia; TNF binding protein;
KW   anti-inflammatory drug; methotrexatess.
XX
```

OS Homo sapiens.
XX
PN WO9824463-A2.
XX
PD 11-JUN-1998.
XX
PF 08-DEC-1997; 97WO-US22733.
XX
PR 09-JUL-1997; 97US-0052023.
PR 06-DEC-1996; 96US-0032587.
PR 23-JAN-1997; 97US-0036355.
PR 07-FEB-1997; 97US-0039315.
XX
PA (AMGE-) AMGEN INC.
XX
PI Bendele AM, Edwards CK, Sennello RM;
XX
DR WPI; 1998-333039/29.
DR N-PSDB; AAV41548.
XX
PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
PT by administering tumour necrosis factor binding protein and at least
PT one additional anti-inflammatory drug, e.g. methotrexate
XX
PS Disclosure; Fig 1; 104pp; English.
XX
CC This is the amino acid sequence of the human tumour necrosis factor
CC receptor type I, used in the method of the invention involving the
CC treatment of acute or chronic inflammatory disease such as leukaemia
CC by administering tumour necrosis factor binding protein and at least
CC one additional anti-inflammatory drug, e.g. methotrexate.
XX
SQ Sequence 161 AA;

Query Match 23.4%; Score 200.5; DB 19; Length 161;
Best Local Similarity 33.6%; Pred. No. 8.5e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

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Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       4 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 63

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
           | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      64 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 122

Qy     124 NTVCS 128
           ||||:
Db     123 NTVCT 127
```

Search completed: December 10, 2002, 15:05:53
Job time : 30.2346 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:46 ; Search time 10.5062 Seconds
(without alignments)
414.479 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	148	4	US-09-411-722-2	Sequence 2, Appli
2	858	100.0	176	4	US-09-411-722-1	Sequence 1, Appli
3	205	23.9	327	4	US-09-290-640-66	Sequence 66, Appl
4	204.5	23.8	285	4	US-08-804-166-6	Sequence 6, Appli
5	204.5	23.8	285	4	US-08-910-991-6	Sequence 6, Appli
6	200.5	23.4	139	4	US-08-706-945D-129	Sequence 129, App
7	200.5	23.4	153	2	US-08-219-237B-4	Sequence 4, Appli
8	200.5	23.4	153	4	US-08-477-347-12	Sequence 12, Appl
9	200.5	23.4	153	4	US-08-476-862-3	Sequence 3, Appli
10	200.5	23.4	153	4	US-08-468-560C-4	Sequence 4, Appli
11	200.5	23.4	154	4	US-08-828-683A-12	Sequence 12, Appl
12	200.5	23.4	161	4	US-09-326-394-2	Sequence 2, Appli
13	200.5	23.4	167	1	US-08-050-319B-2	Sequence 2, Appli
14	200.5	23.4	167	1	US-08-050-319B-57	Sequence 57, Appl
15	200.5	23.4	167	2	US-08-465-982-2	Sequence 2, Appli
16	200.5	23.4	167	2	US-08-465-982-57	Sequence 57, Appl
17	200.5	23.4	197	4	US-08-828-683A-21	Sequence 21, Appl
18	200.5	23.4	256	4	US-08-804-166-2	Sequence 2, Appli
19	200.5	23.4	256	4	US-08-910-991-2	Sequence 2, Appli
20	200.5	23.4	280	3	US-08-974-022-46	Sequence 46, Appl
21	200.5	23.4	280	4	US-08-795-445A-46	Sequence 46, Appl
22	200.5	23.4	280	4	US-08-795-447A-46	Sequence 46, Appl
23	200.5	23.4	280	4	US-08-974-186-46	Sequence 46, Appl
24	200.5	23.4	280	4	US-08-795-446B-46	Sequence 46, Appl
25	200.5	23.4	280	4	US-08-706-945D-132	Sequence 132, App
26	200.5	23.4	307	4	US-08-804-166-4	Sequence 4, Appli
27	200.5	23.4	307	4	US-08-910-991-4	Sequence 4, Appli
28	200.5	23.4	336	4	US-08-804-166-8	Sequence 8, Appli
29	200.5	23.4	336	4	US-08-910-991-8	Sequence 8, Appli
30	200.5	23.4	349	4	US-09-006-353A-13	Sequence 13, Appl
31	200.5	23.4	349	4	US-09-573-986-13	Sequence 13, Appl
32	200.5	23.4	455	1	US-08-050-319B-25	Sequence 25, Appl
33	200.5	23.4	455	1	US-08-321-668-2	Sequence 2, Appli
34	200.5	23.4	455	1	US-08-837-941-2	Sequence 2, Appli
35	200.5	23.4	455	2	US-08-126-016-2	Sequence 2, Appli
36	200.5	23.4	455	2	US-08-465-982-25	Sequence 25, Appl
37	200.5	23.4	455	4	US-08-815-469-5	Sequence 5, Appli
38	200.5	23.4	455	4	US-09-006-353A-3	Sequence 3, Appli
39	200.5	23.4	455	4	US-09-527-236A-5	Sequence 5, Appli
40	200.5	23.4	455	4	US-08-054-970-2	Sequence 2, Appli
41	200.5	23.4	455	4	US-09-565-918-4	Sequence 4, Appli
42	200.5	23.4	455	4	US-09-573-986-3	Sequence 3, Appli
43	199.5	23.3	124	1	US-08-050-319B-4	Sequence 4, Appli
44	199.5	23.3	124	2	US-08-465-982-4	Sequence 4, Appli
45	199.5	23.3	199	1	US-08-050-319B-48	Sequence 48, Appl

ALIGNMENTS

```
RESULT 1
US-09-411-722-2
; Sequence 2, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
;  APPLICANT:  Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION:  NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE:  06501/040001
;  CURRENT APPLICATION NUMBER: US/09/411,722
;  CURRENT FILING DATE:  1999-10-01
;  PRIOR APPLICATION NUMBER:  PCT/JP98/01511
;  PRIOR FILING DATE:  1998-04-01
;  PRIOR APPLICATION NUMBER:  JP 9/099653
;  PRIOR FILING DATE:  1997-04-01
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-411-722-2

  Query Match            100.0%;  Score 858;  DB 4;  Length 148;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-74;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
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Db       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60

Qy      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
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Qy     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
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Db     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148


RESULT 2
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
;  APPLICANT:  Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION:  NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE:  06501/040001
;  CURRENT APPLICATION NUMBER: US/09/411,722
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;  CURRENT FILING DATE:  1999-10-01
;  PRIOR APPLICATION NUMBER:  PCT/JP98/01511
;  PRIOR FILING DATE:  1998-04-01
;  PRIOR APPLICATION NUMBER:  JP 9/099653
;  PRIOR FILING DATE:  1997-04-01
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-411-722-1

  Query Match             100.0%;  Score 858;  DB 4;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-74;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 88

Qy     61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
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Db     89 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 148

Qy    121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
          ||||||||||||||||||||||||||||
Db    149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176


RESULT 3
US-09-290-640-66
; Sequence 66, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT: Marcusson, Eric G.
;  TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
;  FILE REFERENCE: ISPH-0351
;  CURRENT APPLICATION NUMBER: US/09/290,640
;  CURRENT FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-290-640-66

  Query Match             23.9%;  Score 205;  DB 4;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 4e-12;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy      9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
          || :| ||    ||: |  |      ||:       |  |  |  :  |::    |  |:
Db     43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy     68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
          ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db    103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy    126 VCSSSVSNPRNWLFLLMLIVFCI 148
            |     :||| |:|| ::|  |
Db    160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 4
US-08-804-166-6
; Sequence 6, Application US/08804166
; Patent No. 6193972
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011,936
;      FILING DATE:  20 February 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  285 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-804-166-6

  Query Match             23.8%;  Score 204.5;  DB 4;  Length 285;
  Best Local Similarity   34.4%;  Pred. No. 3.8e-12;
  Matches   43;  Conservative   15;  Mismatches   60;  Indels    7;  Gaps    4;

Qy     10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
          || |:|    |:| :||  |  ||:   |  |     | :|  |:||  :| |  |  ||
Db     26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Qy     67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  || |  |  |   |
Db     86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNG-TVHLSCQEKQ 144

Qy    124 NTVCS 128
            ||||:
Db    145 NTVCT 149


RESULT 5
US-08-910-991-6
; Sequence 6, Application US/08910991
; Patent No. 6194177
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,991
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:  20 February 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/011,936
;      FILING DATE:  20 February 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  CAMPBELL=2B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  285 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-910-991-6

  Query Match             23.8%;  Score 204.5;  DB 4;  Length 285;
  Best Local Similarity   34.4%;  Pred. No. 3.8e-12;
  Matches   43;  Conservative   15;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db      26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  || | |  |   |
Db      86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNG-TVHLSCQEKQ 144

Qy     124 NTVCS 128
           ||||:
Db     145 NTVCT 149


RESULT 6
US-08-706-945D-129
; Sequence 129, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Lacey, David
;  APPLICANT:  Calzone, Frank
;  APPLICANT:  Chang, Ming-Shi
;  TITLE OF INVENTION: Osteoprotegerin
;  FILE REFERENCE: A-378CIP
;  CURRENT APPLICATION NUMBER: US/08/706,945D
;  CURRENT FILING DATE:  1996-09-03
;  PRIOR APPLICATION NUMBER: 08/577,788
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-706-945D-129

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 139;
  Best Local Similarity   33.6%;  Pred. No. 4.1e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       1 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 60

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:.  |  | |:   | :|  :    |  |: |  |  |   |
Db      61 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 119

Qy     124 NTVCS 128
           ||||:
Db     120 NTVCT 124


RESULT 7
US-08-219-237B-4
; Sequence 4, Application US/08219237B
; Patent No. 5874546
;  GENERAL INFORMATION:
;    APPLICANT:  NAGATA, Shigekazu
;    APPLICANT:  ITOH, Naoto
;    APPLICANT:  YONEHARA, Shin
;    TITLE OF INVENTION:  DNA Coding for Human Cell Surface Antigen
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James W. Hellwege
;      STREET:  P.O. Box 2266 Eads Station
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/219,237B
;      FILING DATE:  28-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,129
;      FILING DATE:  22-APR-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James W. Hellwege
;      REGISTRATION NUMBER:  28,808
;      REFERENCE/DOCKET NUMBER:  516762
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  153 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-219-237B-4

  Query Match             23.4%;  Score 200.5;  DB 2;  Length 153;
  Best Local Similarity   33.6%;  Pred. No. 4.6e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 8
```

```
US-08-477-347-12
; Sequence 12, Application US/08477347
; Patent No. 6232446
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    TITLE OF INVENTION:  TNF LIGANDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,347
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/115,685
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 106271
;      FILING DATE:  08-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, G. Kevin
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  WALLACH=10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  153 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-347-12

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 153;
  Best Local Similarity   33.6%;  Pred. No. 4.6e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 9
US-08-476-862-3
; Sequence 3, Application US/08476862
; Patent No. 6262239
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,862
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107267
;      FILING DATE:  12-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  153 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-476-862-3

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 153;
  Best Local Similarity   33.6%;  Pred. No. 4.6e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 10
US-08-468-560C-4
; Sequence 4, Application US/08468560C
; Patent No. 6270998
;  GENERAL INFORMATION:
;    APPLICANT:  NAGATA, Shigekazu
;    APPLICANT:  ITOH, Naoto
```

```
;    APPLICANT:  YONEHARA, Shin
;    TITLE OF INVENTION:  DNA CODING FOR HUMAN CELL SURFACE
;    TITLE OF INVENTION:  ANTIGEN
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH, LLP.
;      STREET:  P.O. BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,560C
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR., GERLAD M.
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  20-4393P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  153 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-468-560C-4

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 153;
  Best Local Similarity   33.6%;  Pred. No. 4.6e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 11
US-08-828-683A-12
; Sequence 12, Application US/08828683A
; Patent No. 6469144
;  GENERAL INFORMATION:
;       APPLICANT: Ashkenazi, Avi J.
;       TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/828,683A
;            FILING DATE: 31-Mar-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/625328
;            FILING DATE: 1-Apr-1996
;            APPLICATION NUMBER: 08/710802
;            FILING DATE: 23-Sep-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P1007P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 154 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-828-683A-12

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 154;
  Best Local Similarity   33.6%;  Pred. No. 4.6e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 61

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      62 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 120

Qy     124 NTVCS 128
           ||||:
Db     121 NTVCT 125


RESULT 12
US-09-326-394-2
; Sequence 2, Application US/09326394
; Patent No. 6306820
;  GENERAL INFORMATION:
;    APPLICANT:  Bendele, Alison M.
;    APPLICANT:  Sennello, Regina M.
;    APPLICANT:  Edwards, Carl K.
;    TITLE OF INVENTION:  COMBINATION THERAPY USING A TNF BINDING
;    TITLE OF INVENTION:  PROTEIN FOR TREATING TNF-MEDIATED DISEASES
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/326,394
;      FILING DATE:  08-DEC-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,587
;      FILING DATE:  06-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/036,355
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;      FILING DATE:  23-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,315
;      FILING DATE:  07-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/052,023
;      FILING DATE:  09-JUL-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zindrick, Thomas K.
;      REGISTRATION NUMBER:  32,185
;      REFERENCE/DOCKET NUMBER:  A-430D
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  161 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-326-394-2

  Query Match             23.4%;  Score 200.5;  DB 4;  Length 161;
  Best Local Similarity   33.6%;  Pred. No. 4.8e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

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Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
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Db      64 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 122

Qy     124 NTVCS 128
           ||||:
Db     123 NTVCT 127


RESULT 13
US-08-050-319B-2
; Sequence 2, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319B
;      FILING DATE:  10-May-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-319B-2

  Query Match             23.4%;  Score 200.5;  DB 1;  Length 167;
  Best Local Similarity   33.6%;  Pred. No. 5e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |      | :|  |:||  :| |  |  ||
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Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
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Qy     124 NTVCS 128
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Db     163 NTVCT 167


RESULT 14
US-08-050-319B-57
; Sequence 57, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319B
;      FILING DATE:  10-May-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-319B-57

  Query Match             23.4%;  Score 200.5;  DB 1;  Length 167;
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  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
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Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
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Qy     124 NTVCS 128
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Db     163 NTVCT 167


RESULT 15
US-08-465-982-2
; Sequence 2, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-982-2

  Query Match             23.4%;  Score 200.5;  DB 2;  Length 167;
  Best Local Similarity   33.6%;  Pred. No. 5e-12;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
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Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
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GenCore version 5.1.3

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Run on: December 10, 2002, 15:05:57 ; Search time 6.85185 Seconds
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350.834 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	148	10	US-09-855-266A-2	Sequence 2, Appli
2	858	100.0	176	10	US-09-855-266A-1	Sequence 1, Appli
3	213.5	24.9	162	10	US-09-798-789-13	Sequence 13, Appl
4	212.5	24.8	123	10	US-09-855-266A-13	Sequence 13, Appl
5	209	24.4	461	9	US-09-898-234-15	Sequence 15, Appl
6	209	24.4	461	9	US-09-899-429A-25	Sequence 25, Appl
7	209	24.4	461	10	US-09-899-422-15	Sequence 15, Appl
8	207.5	24.2	162	10	US-09-798-789-15	Sequence 15, Appl
9	205	23.9	204	10	US-09-948-018-18	Sequence 18, Appl
10	205	23.9	327	10	US-09-802-669-66	Sequence 66, Appl
11	204.5	23.8	162	10	US-09-798-789-20	Sequence 20, Appl
12	204.5	23.8	285	10	US-09-756-186-6	Sequence 6, Appli
13	203.5	23.7	162	10	US-09-798-789-19	Sequence 19, Appl
14	202.5	23.6	162	10	US-09-798-789-11	Sequence 11, Appl
15	201.5	23.5	162	10	US-09-798-789-14	Sequence 14, Appl
16	200.5	23.4	153	10	US-09-800-909-3	Sequence 3, Appli
17	200.5	23.4	153	10	US-09-884-987-4	Sequence 4, Appli
18	200.5	23.4	153	10	US-09-800-908-12	Sequence 12, Appl
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20	200.5	23.4	161	9	US-09-899-429A-4	Sequence 4, Appli
21	200.5	23.4	161	10	US-09-899-422-4	Sequence 4, Appli
22	200.5	23.4	161	10	US-09-907-263-2	Sequence 2, Appli
23	200.5	23.4	162	9	US-09-899-429A-6	Sequence 6, Appli
24	200.5	23.4	162	10	US-09-798-789-9	Sequence 9, Appli
25	200.5	23.4	162	10	US-09-798-789-21	Sequence 21, Appl
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29	200.5	23.4	183	9	US-09-899-429A-10	Sequence 10, Appl
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31	200.5	23.4	200	9	US-09-899-429A-12	Sequence 12, Appl
32	200.5	23.4	201	9	US-09-899-429A-14	Sequence 14, Appl
33	200.5	23.4	211	9	US-09-899-429A-8	Sequence 8, Appli
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35	200.5	23.4	307	10	US-09-756-186-4	Sequence 4, Appli
36	200.5	23.4	336	10	US-09-756-186-8	Sequence 8, Appli
37	200.5	23.4	349	10	US-09-826-212-13	Sequence 13, Appl
38	200.5	23.4	349	10	US-09-935-727-15	Sequence 15, Appl
39	200.5	23.4	371	9	US-09-898-234-12	Sequence 12, Appl
40	200.5	23.4	371	10	US-09-899-422-12	Sequence 12, Appl
41	200.5	23.4	455	9	US-09-898-234-2	Sequence 2, Appli
42	200.5	23.4	455	9	US-09-898-234-17	Sequence 17, Appl
43	200.5	23.4	455	9	US-09-756-854-5	Sequence 5, Appli
44	200.5	23.4	455	9	US-09-899-429A-2	Sequence 2, Appli
45	200.5	23.4	455	9	US-09-899-429A-27	Sequence 27, Appl

ALIGNMENTS

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RESULT 1
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
;  APPLICANT: Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE: 06501-040002
;  CURRENT APPLICATION NUMBER: US/09/855,266A
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/411,722
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: PCT/JP98/01511
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: JP 9/099653
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-855-266A-2

  Query Match             100.0%;  Score 858;  DB 10;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-64;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60

Qy      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
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Qy     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
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Db     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
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RESULT 2
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
;  APPLICANT: Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE: 06501-040002
;  CURRENT APPLICATION NUMBER: US/09/855,266A
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/411,722
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: PCT/JP98/01511
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: JP 9/099653
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-855-266A-1

  Query Match             100.0%;  Score 858;  DB 10;  Length 176;
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Qy    121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
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Db    149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176


RESULT 3
US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-13

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Qy     10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
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Db      5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRDCLQCS 64

Qy     67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
          | |    |  : |:   |  | |:   | :|| :    |  |: | |  |   |
Db     65 QCKKHDGQVEISSCTVDRDTVCGCRKNQYRHYDHENRFYCFNCSLCLNG-TVHLSCQEKQ 123

Qy    124 NTVCS 128
          ||||:
Db    124 NTVCT 128


RESULT 4
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
;  APPLICANT: Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE: 06501-040002
;  CURRENT APPLICATION NUMBER: US/09/855,266A
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/411,722
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: PCT/JP98/01511
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: JP 9/099653
;. PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-855-266A-13

  Query Match             24.8%;  Score 212.5;  DB 10;  Length 123;
  Best Local Similarity   35.7%;  Pred. No. 3.2e-11;
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Qy     10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
          || |:|   ::| :||  |  ||:: : |  |     | :|  ||||   | |  |  |
Db      1 CPGGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 60

Qy     67 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
          || |: : |  : | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     61 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 117

Qy    122 TANTVC 127
          | ||||
Db    118 TQNTVC 123


RESULT 5
US-09-898-234-15
; Sequence 15, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;. TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
```

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;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-898-234-15

  Query Match           24.4%;  Score 209;  DB 9;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 2.1e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  ::| | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN----------WL 138
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148
            | :|   ||
Db     221 GLCLLFFICI 230


RESULT 6
US-09-899-429A-25
; Sequence 25, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-899-429A-25

  Query Match           24.4%;  Score 209;  DB 9;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 2.1e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  ::| | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN----------WL 138
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148
            | :|   ||
Db     221 GLCLLFFICI 230


RESULT 7
US-09-899-422-15
; Sequence 15, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-899-422-15

  Query Match           24.4%;  Score 209;  DB 10;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 2.1e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  ::| | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN----------WL 138
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148
            | :|   ||
Db     221 GLCLLFFICI 230
```

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RESULT 8
US-09-798-789-15
; Sequence 15, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-15

  Query Match             24.2%;  Score 207.5;  DB 10;  Length 162;
  Best Local Similarity   34.4%;  Pred. No. 1.1e-10;
  Matches   43;  Conservative   17;  Mismatches   58;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  | |||
Db       5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENWLRRCLLCS 64

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |::  |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      65 KCRKEEGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 123

Qy     124 NTVCS 128
           ||||:
Db     124 NTVCT 128


RESULT 9
US-09-948-018-18
; Sequence 18, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
;  APPLICANT: Theill et al
;  TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
;  FILE REFERENCE: 01017/37677
;  CURRENT APPLICATION NUMBER: US/09/948,018
;  CURRENT FILING DATE:  2001-09-05
;  PRIOR APPLICATION NUMBER: US 60/230,191
;  PRIOR FILING DATE: 2000-09-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-948-018-18

  Query Match             23.9%;  Score 205;  DB 10;  Length 204;
  Best Local Similarity   31.5%;  Pred. No. 2.1e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |      ||:      |  |  |  :  |:.    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
           |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 10
US-09-802-669-66
; Sequence 66, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
;  FILE REFERENCE: ISPH-545
;  CURRENT APPLICATION NUMBER: US/09/802,669
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: US 09/665,615
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 09/290,640
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-802-669-66

  Query Match             23.9%;  Score 205;  DB 10;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 3.2e-10;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
           |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 11
US-09-798-789-20
; Sequence 20, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-20
```

Query Match 23.8%; Score 204.5; DB 10; Length 162;
Best Local Similarity 33.6%; Pred. No. 1.9e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

Qy 10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
Db 5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 64

Qy 67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
Db 65 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYQSENLFQCFNCSLCLNG-TVHLSCQEKQ 123

Qy 124 NTVCS 128
Db 124 NTVCT 128

RESULT 12
US-09-756-186-6
; Sequence 6, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-186-6

Query Match 23.8%; Score 204.5; DB 10; Length 285;
Best Local Similarity 34.4%; Pred. No. 3.1e-10;
Matches 43; Conservative 15; Mismatches 60; Indels 7; Gaps 4;

Qy 10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
Db 26 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 85

Qy 67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
Db 86 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCTLCLNG-TVHLSCQEKQ 144

Qy 124 NTVCS 128
Db 145 NTVCT 149

RESULT 13
US-09-798-789-19
; Sequence 19, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-19

Query Match 23.7%; Score 203.5; DB 10; Length 162;
Best Local Similarity 33.6%; Pred. No. 2.3e-10;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

Qy 10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
Db 5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 64

Qy 67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
Db 65 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYKSENLFQCFNCSLCLNG-TVHLSCQEKQ 123

Qy 124 NTVCS 128
Db 124 NTVCT 128

RESULT 14
US-09-798-789-11
; Sequence 11, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-11

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  Query Match             23.6%;  Score 202.5;  DB 10;  Length 162;
  Best Local Similarity   33.6%;  Pred. No. 2.7e-10;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRTCLSCS 64

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            | |:   |  : |:   |  | |:   | :|  :    |  |: |  |   |   |
Db      65 KCLKEMGQVEISSCTVDRDTVCGCRKNQYRHYASENKFQCFNCSLCLNG-TVHLSCQEKQ 123

Qy     124 NTVCS 128
           ||||:
Db     124 NTVCT 128


RESULT 15
US-09-798-789-14
; Sequence 14, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-14

  Query Match             23.5%;  Score 201.5;  DB 10;  Length 162;
  Best Local Similarity   33.6%;  Pred. No. 3.3e-10;
  Matches   42;  Conservative   17;  Mismatches   59;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  |  ||
Db       5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRQCLSCS 64

Qy      67 TCDK--DQNMVADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            |:|   |  :: |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      65 KCEKWMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFKCFNCSLCLNG-TVHLSCQEKQ 123

Qy     124 NTVCS 128
           ||||:
Db     124 NTVCT 128


Search completed: December 10, 2002, 15:08:42
Job time : 7.85185 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:21 ; Search time 13.2469 Seconds
(without alignments)
1074.054 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215.5	25.1	454	1	GQMST1	tumor necrosis fac
2	210	24.5	461	1	GQRTT1	tumor necrosis fac
3	205	23.9	327	2	A46484	apoptosis-mediatin
4	200.5	23.4	348	2	T28623	hypothetical prote
5	200.5	23.4	349	2	D72175	G2R protein - vari
6	200.5	23.4	349	2	D36858	gene G4R protein -
7	200.5	23.4	455	1	GQHUT1	tumor necrosis fac
8	193.5	22.6	461	2	JC4302	tumor necrosis fac
9	190	22.1	324	2	JC2395	Fas antigen precur
10	189.5	22.1	335	2	A40036	apoptosis-mediatin
11	177.5	20.7	427	1	GQHUN	nerve growth facto
12	177	20.6	314	2	I37383	FAS soluble protei
13	177	20.6	651	2	JC7705	death receptor-6 -
14	168.5	19.6	425	1	A26431	nerve growth facto
15	164.5	19.2	326	1	GQVZML	T2 protein - myxom
16	163.5	19.1	416	1	JN0006	nerve growth facto
17	156	18.2	325	2	B43692	T2 protein - rabbi
18	148.5	17.3	461	1	A35356	tumor necrosis fac
19	148	17.2	250	1	A49053	CD27 antigen precu
20	146	17.0	435	2	I54182	tumor necrosis fac
21	144.5	16.8	474	2	B38634	tumor necrosis fac
22	143.5	16.7	260	1	A46517	CD27 antigen precu
23	143	16.7	271	2	S12783	OX40 antigen precu
24	142.5	16.6	459	2	I48854	gene murine tumour
25	138	16.1	595	2	A42086	CD30 antigen precu
26	136.5	15.9	1790	1	MMFFB1	laminin beta-1 cha
27	135.5	15.8	493	2	JC5486	membrane glycoprot
28	134	15.6	277	2	I37552	OX40 homolog - hum
29	134	15.6	305	2	A46476	B cell-associated
30	130	15.2	256	2	B32393	T-cell antigen 4-1
31	126.5	14.7	1193	2	A44018	laminin B2t chain
32	125.5	14.6	1192	2	S69000	laminin gamma 2 ch
33	124	14.5	1827	2	T34288	hypothetical prote
34	123.5	14.4	255	2	I38426	lymphocyte activat
35	122	14.2	272	2	I48700	gene ox40 protein
36	122	14.2	435	2	S40993	hypothetical prote
37	121.5	14.2	1274	2	T42017	cysteine rich prot
38	120	14.0	4391	2	A38096	perlecan precursor
39	119.5	13.9	1609	1	MMHUB2	laminin gamma-1 ch
40	118	13.8	570	2	T37314	probable kexin (EC
41	118	13.8	942	2	D87803	protein bli-4D [im
42	117	13.6	1548	2	S34583	serine proteinase
43	116	13.5	557	2	A48434	variant-specific s
44	115.5	13.5	1372	2	T25933	hypothetical prote
45	115.5	13.5	1808	2	T15099	hypothetical prote

ALIGNMENTS

RESULT 1
GQMST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A;Reference number: I54532; MUID:94245292; PMID:8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis fact
A;Reference number: I57826; MUID:93156721; PMID:8381516

```
A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             25.1%;  Score 215.5;  DB 1;  Length 454;
  Best Local Similarity   28.1%;  Pred. No. 1.2e-09;
  Matches   52;  Conservative   23;  Mismatches   61;  Indels   49;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :|| |  ||:: : |  |     | :|  |||   | | |  |
Db      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 103

Qy      67 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |: : |  : | |  | | |    |  : |   |  |: | |  |   |
Db     104 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN-----WLFLLML 143
           | ||||:                                ::|:||::      | |::|
Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVIL 220

Qy     144 IVFCI 148
           :  |:
Db     221 LGLCL 225


RESULT 2
GQRTT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             24.5%;  Score 210;  DB 1;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 3.2e-09;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |  :  || |  ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  :: | |  | | |    |  : |   |  |: | |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN-----WL 138
             ||||:                               .::|:||::      :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148
           | :|   ||
Db     221 GLCLLFFICI 230


RESULT 3
A46484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki
J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Accession: A46484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <WAT>
A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A;Experimental source: BAM3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable elem
A;Reference number: A47254; MUID:93189576; PMID:7680478
A;Accession: A47254
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>

  Query Match             23.9%;  Score 205;  DB 2;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 6.1e-09;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
           |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 4
T28623
```

hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 23.4%; Score 200.5; DB 2; Length 348;
Best Local Similarity 36.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 16; Mismatches 55; Indels 7; Gaps 5;

Qy 10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
Db 31 CKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 89

Qy 69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
Db 90 NSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSVGDV 147

Qy 126 VCS 128
Db 148 ICS 150

RESULT 5
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 23.4%; Score 200.5; DB 2; Length 349;
Best Local Similarity 36.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 16; Mismatches 55; Indels 7; Gaps 5;

Qy 10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
Db 32 CKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 90

Qy 69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
Db 91 NSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSVGDV 148

Qy 126 VCS 128
Db 149 ICS 151

RESULT 6
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protect
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 23.4%; Score 200.5; DB 2; Length 349;
Best Local Similarity 36.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 16; Mismatches 55; Indels 7; Gaps 5;

Qy 10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
Db 32 CKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 90

Qy 69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
Db 91 NSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSVGDV 148

Qy 126 VCS 128
Db 149 ICS 151

RESULT 7
GQHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231;
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to
A;Reference number: A38208; MUID:92250049; PMID:1315717
A;Accession: A38208
A;Molecule type: DNA
A;Residues: 1-455 <FUC>
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less

Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
A;Reference number: A34899; MUID:90235284; PMID:2158862
A;Accession: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <LOE>
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A;Experimental source: placenta
A;Note: part of this sequence, including the amino end of the mature protein, confirmed
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.
Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
A;Reference number: A34900; MUID:90235285; PMID:2158863
A;Accession: A34900
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: A36555
A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
A;Reference number: A38281; MUID:91017509; PMID:2170974
A;Accession: A38281
A;Molecule type: mRNA
A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <NOP>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R;Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A;Reference number: A38258; MUID:91062364; PMID:2174164
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989

A;Title: Isolation and characterization of a tumor necrosis factor binding protein fr
A;Reference number: A60594; MUID:89171156; PMID:2924890
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purifie
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.4%; Score 200.5; DB 1; Length 455;
Best Local Similarity 33.6%; Pred. No. 1.7e-08;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

```
Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :||  |  ||::  |  |     | :|  |:||  :| |  |  ||
Db      44 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 103

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
           | |:  |  : |:  |  | |:  | :|  :   |  |: | |  |  |
Db     104 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 162

Qy     124 NTVCS 128
           ||||:
Db     163 NTVCT 167
```

RESULT 8
JC4302
tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645; PMID:7590278
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753

```
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             22.6%;  Score 193.5;  DB 2;  Length 461;
  Best Local Similarity   32.3%;  Pred. No. 6e-08;
  Matches   41;  Conservative   17;  Mismatches   58;  Indels   11;  Gaps    5;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:  :||  |  ||::   |  |     | :|  ||||  :| |  |  ||
Db      44 CPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCS 103

Qy      67 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
             |  : : |  : |:   |  | |   |   |: :  |   |  |: || |  |   |
Db     104 KCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLF--QCLNCSLCPNG-TVQLPCLE 160

Qy     122 TANTVCS 128
             :|:|:
Db     161 KQDTICN 167


RESULT 9
JC2395
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat live
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62,'RFT' <KI2>
A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <MAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>

  Query Match             22.1%;  Score 190;  DB 2;  Length 324;
  Best Local Similarity   30.7%;  Pred. No. 8.7e-08;
  Matches   46;  Conservative   22;  Mismatches   64;  Indels   18;  Gaps    8;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT----FTGKDNGLHDCEL 64
           || :| ||    ||: |  |       |    | |    ||| |    :| : :    |
Db      43 NCSEGLYQVGPFCCQPCQPGERKVKDCT---TSGGAPTCHPCTEGEEYTDRKHYSDKCRR 99

Qy      65 CSTCDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGI-PVLQECNS 121
              |: ||:   :  :  |: | : || |:   :| :    : |  || |  |:  :|: |
Db     100 CAFCDEGHGLEVETNCTRTQNTKCRCKEN-FYCNASLCDHCYHCTSC--GLEDILEPCTR 156

Qy     122 TANTVCSSSVSNPR-NWLFLL----MLIVF 146
           |:|| |    || :  || :|    :| ||
Db     157 TSNTKCKKQSSNYKLLWLLILPGLAILFVF 186


RESULT 10
A40036
apoptosis-mediating surface antigen Fas precursor - human
N;Alternate names: surface antigen APO-1
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40036; S24543; A38142
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Ha
Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m
A;Reference number: A40036; MUID:91309137; PMID:1713127
A;Accession: A40036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <ITD>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A;Reference number: S24543
A;Accession: S24543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <KRA>
A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R;Dehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; R
J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APD-1 cell surface antigen, a memb
A;Reference number: A38142; MUID:92268122; PMID:1375228
A;Accession: A38142
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-134,'Q',136-335 <OEH>
A;Experimental source: SKW6.4 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse
C;Genetics:
A;Gene: GDB:APT1
A;Cross-references: GDB:132671; DMIM:134637
A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
C;Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4>
F;174-190/Domain: transmembrane #status predicted <TMM>

  Query Match             22.1%;  Score 189.5;  DB 2;  Length 335;
  Best Local Similarity   30.9%;  Pred. No. 9.8e-08;
  Matches   42;  Conservative   19;  Mismatches   68;  Indels    7;  Gaps    5;

Qy      12 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 70
           :| :     | | || |      | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109

Qy      71 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 128
              :  :  |: | : || |:   :: :    | | ||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     129 SSVSNPR-NWLFLLML 143
           |     || ||:|
Db     167 EEGSRSNLGWLCLLLL 182


RESULT 11
GQHUN
nerve growth factor receptor precursor, low affinity [validated] - human
```

```
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factc
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleoti
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             20.7%;  Score 177.5;  DB 1;  Length 427;
  Best Local Similarity   33.6%;  Pred. No. 9.7e-07;
  Matches   40;  Conservative    9;  Mismatches   65;  Indels    5;  Gaps    3;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTC 68
           || | |  :  ||| |  |  |  ||     | || |    ||:   :    |: |: |
Db      32 CPTGLYTHSGECCKACNLGEGVAQPCGA--NQTVCEPCLDSVTFSDVVSATEPCKPCTEC 89

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC 127
             |:| | |    |  | |  |  ||  :    |  |  |  |  ::  |    ||||
Db      90 VGLQSMSAPCVEADDAVCRCAYG--YYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVC 146
```

```
RESULT 12
I37383
FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I37383
R;Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule
A;Reference number: I37383; MUID:95181785; PMID:7533181
A;Accession: I37383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539

  Query Match             20.6%;  Score 177;  DB 2;  Length 314;
  Best Local Similarity   30.1%;  Pred. No. 8.6e-07;
  Matches   37;  Conservative   18;  Mismatches   62;  Indels    6;  Gaps    4;

Qy      12 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 70
           :| :     | | || |      | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109

Qy      71 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 128
           :  :  |: | : || |:   :: :    | | |||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     129 SSV 131
             |
Db     167 EEV 169


RESULT 13
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belo
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match             20.6%;  Score 177;  DB 2;  Length 651;
  Best Local Similarity   29.8%;  Pred. No. 1.4e-06;
  Matches   39;  Conservative   22;  Mismatches   58;  Indels   12;  Gaps    4;

Qy       4 ESYSFNCPDGEY------QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDN 57
           |  : : | |:|       : :: |  ||:||:|   |     |  :|  |  ||||  :|
Db      28 EQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC-TKSTLRECSPCPDGTFTKHEN 86

Qy      58 GLHDCELC-STCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVL 116
           |:  |  |   |:        |:| :||:| |  | :    :  ::| | | || |  |
Db      87 GIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF----QINDTCVPYTVCPVGWGVR 142

Qy     117 QECNSTANTVC 127
           ::   | :  |
Db     143 KKGTETEDVRC 153
```

```
RESULT 14
A26431
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.6%;  Score 168.5;  DB 1;  Length 425;
  Best Local Similarity   32.8%;  Pred. No. 4.8e-06;
  Matches   39;  Conservative   10;  Mismatches   65;  Indels    5;  Gaps    3;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTC 68
           |  | |  :  ||| |  |  |  ||     |  || |    ||:   :    |: |: |
Db      33 CSTGLYTHSGECCKACNLGEGVAQPCGA--NQTVCEPCLDNVTFSDVVSATEPCKPCTEC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC 127
             |:| | |    |  | |  |  ||  :    |  |: |  |  ::  |    ||||
Db      91 LGLQSMSAPCVEADDAVCRCAYG--YYQDEETGHCEACSVCEVGSGLVFSCQDKQNTVC 147


RESULT 15
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.2%;  Score 164.5;  DB 1;  Length 326;
  Best Local Similarity   31.7%;  Pred. No. 8.1e-06;
  Matches   39;  Conservative   13;  Mismatches   64;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELC-STC 68
           |   :|: : :|| :|| |::    |  | :   |  |   |||   |    |  |   |
Db      28 CRGNDYEKDGLCCTSCPPGSYASRLCG-PGSDTVCSPCKNETFTASTNHAPACVSCRGRC 86

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
             :    |  | || |:|  | |     |  | || |   ||| |  |      | :
Db      87 TGHLSESQSCDKTRDRVCDCSAGNYCL-LKGQEGCRICAPKTKCPAGYGVSGH-TRTGDV 144

Qy     126 VCS 128
           :|:
Db     145 LCT 147


Search completed: December 10, 2002, 15:07:52
Job time : 14.2469 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 14:57:06 ; Search time 7.30864 Seconds
(without alignments)
839.896 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	176	1	TR23_MOUSE	Q9er63 mus musculu
2	641	74.7	180	1	TR22_MOUSE	Q9er62 mus musculu
3	226.5	26.4	332	1	TNR6_PIG	O77736 sus scrofa
4	219.5	25.6	323	1	TNR6_BOVIN	P51867 bos taurus
5	215.5	25.1	454	1	TR1A_MOUSE	P25118 mus musculu
6	211.5	24.7	351	1	CRMB_COWPX	O73559 cowpox viru
7	210	24.5	461	1	TR1A_RAT	P22934 rattus norv
8	208.5	24.3	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
9	205	23.9	327	1	TNR6_MOUSE	P25446 mus musculu
10	200.5	23.4	349	1	CRMB_VARV	P34015 variola vir
11	200.5	23.4	455	1	TR1A_HUMAN	P19438 homo sapien
12	193.5	22.6	461	1	TR1A_PIG	P50555 sus scrofa
13	190	22.1	324	1	TNR6_RAT	Q63199 rattus norv
14	189.5	22.1	335	1	TNR6_HUMAN	P25445 homo sapien
15	186.5	21.7	471	1	TR1A_BOVIN	O19131 bos taurus
16	177.5	20.7	427	1	TR16_HUMAN	P08138 homo sapien
17	169.5	19.8	417	1	TR16_MOUSE	Q9z0w1 mus musculu
18	168.5	19.6	425	1	TR16_RAT	P07174 rattus norv
19	167	19.5	283	1	TR14_HUMAN	Q92956 homo sapien
20	164.5	19.2	326	1	VT2_MYXVL	P29825 myxoma viru
21	164.5	19.2	386	1	T10D_HUMAN	Q9ubn6 homo sapien
22	164.5	19.2	417	1	TR12_HUMAN	Q93038 h tumor nec
23	164.5	19.2	655	1	TR21_MOUSE	Q9epu5 mus musculu
24	163.5	19.1	416	1	TR16_CHICK	P18519 gallus gall
25	163.5	19.1	655	1	TR21_HUMAN	O75509 homo sapien
26	160	18.6	259	1	T10C_HUMAN	O14798 h tumor nec
27	156	18.2	325	1	VT2_SFVKA	P25943 shope fibro
28	156	18.2	468	1	T10A_HUMAN	O00220 homo sapien
29	151	17.6	381	1	T10B_MOUSE	Q9qzm4 mus musculu
30	150.5	17.5	415	1	TNR3_MOUSE	P50284 mus musculu
31	150	17.5	416	1	TR19_MOUSE	Q9j113 mus musculu
32	148.5	17.3	300	1	TR6B_HUMAN	O95407 homo sapien
33	148.5	17.3	461	1	TR1B_HUMAN	P20333 homo sapien
34	148	17.2	250	1	TNR7_MOUSE	P41272 mus musculu
35	147.5	17.2	401	1	T11B_MOUSE	O08712 mus musculu
36	146.5	17.1	401	1	T11B_RAT	O08727 rattus norv
37	146	17.0	435	1	TNR3_HUMAN	P36941 homo sapien
38	144.5	16.8	474	1	TR1B_MOUSE	P25119 mus musculu
39	144	16.8	401	1	T11B_HUMAN	O00300 homo sapien
40	143.5	16.7	260	1	TNR7_HUMAN	P26842 homo sapien
41	143	16.7	271	1	TNR4_RAT	P15725 rattus norv
42	143	16.7	498	1	TNR8_MOUSE	Q60846 mus musculu
43	138	16.1	595	1	TNR8_HUMAN	P28908 homo sapien
44	136.5	15.9	1790	1	LMB1_DROME	P11046 drosophila
45	135.5	15.8	493	1	TNR8_RAT	P97525 rattus norv

ALIGNMENTS

RESULT 1
TR23_MOUSE
ID TR23_MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
DE factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN TNFRSF23 OR TNFRSF1AL1 OR TNFRH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pan G., Mao W., Risser P.;
RT "Characterization of SOB, a member of the TNFR family.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC ---

CC ---
DR EMBL; AJ278264; CAC16405.1; -.
DR EMBL; AJ276505; CAC27352.1; -.
DR EMBL; AY046550; AAL05072.1; -.
DR HSSP; P19438; 1EXT.
DR MGD; MGI:1930269; Tnfrsf23.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).
FT REPEAT 37 72 TNFR-CYS 1.
FT REPEAT 74 114 TNFR-CYS 2.

```
FT   REPEAT      115    155       TNFR-CYS 3.
FT   DISULFID     38     49       BY SIMILARITY.
FT   DISULFID     50     63       BY SIMILARITY.
FT   DISULFID     53     72       BY SIMILARITY.
FT   DISULFID     75     90       BY SIMILARITY.
FT   DISULFID     93    106       BY SIMILARITY.
FT   DISULFID     96    114       BY SIMILARITY.
FT   DISULFID    116    131       BY SIMILARITY.
FT   DISULFID    134    147       BY SIMILARITY.
FT   DISULFID    137    155       BY SIMILARITY.
FT   CARBOHYD    148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   176 AA;  19594 MW;  EE30D617F49DDB7D CRC64;

  Query Match             100.0%;  Score 858;  DB 1;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-66;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      29 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 88

Qy      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 148

Qy     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148
           ||||||||||||||||||||||||||||
Db     149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176


RESULT 2
TR22_MOUSE
ID   TR22_MOUSE     STANDARD;      PRT;   180 AA.
AC   Q9ER62; Q9CZA4; Q8VHB9;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis
DE   factor receptor p60 homolog 2) (TNF receptor family member SOBa).
GN   TNFRSF22 OR TNFRSF1AL2 OR TNFRH2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX   MEDLINE=20519229; PubMed=11063728;
RA   Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA   Lane N., Reik W., Walter J.;
RT   "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT   implications for a novel imprinting centre and extended imprinting.";
RL   Hum. Mol. Genet. 9:2691-2706(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Risser P., Mao W., Baldwin D.T., Pan G.;
RT   "Characterization of SOBa, a murine member of the TNFR family.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ278265; CAC16406.1; -.
DR   EMBL; AJ276505; CAC27353.1; -.
DR   EMBL; AY046551; AAL05073.1; -.
DR   EMBL; AK012838; BAB28502.1; -.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1930270; Tnfrsf22.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     41       SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       42    180       EXTRACELLULAR (POTENTIAL).
FT   REPEAT       47     82       TNFR-CYS 1.
FT   REPEAT       84    124       TNFR-CYS 2.
FT   REPEAT      125    165       TNFR-CYS 3.
FT   DISULFID     48     59       BY SIMILARITY.
FT   DISULFID     60     73       BY SIMILARITY.
FT   DISULFID     63     82       BY SIMILARITY.
FT   DISULFID     85    100       BY SIMILARITY.
FT   DISULFID    103    116       BY SIMILARITY.
FT   DISULFID    106    124       BY SIMILARITY.
FT   DISULFID    126    141       BY SIMILARITY.
FT   DISULFID    144    157       BY SIMILARITY.
FT   DISULFID    147    165       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     12     12       L -> V (IN REF. 3).
FT   CONFLICT    171    180       RRSASVAWPI -> NPRNRLFLLL (IN REF. 2).
SQ   SEQUENCE   180 AA;  20226 MW;  F8F56E165ADD53FA CRC64;

  Query Match             74.7%;  Score 641;  DB 1;  Length 180;
  Best Local Similarity   84.8%;  Pred. No. 3.5e-48;
  Matches  112;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
           || | :|| || ||| | ||||| | :||||||||:||||||||||||||||| ||| |
Db      39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD 98

Qy      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
            | ||||||||| ||||||||||||:|: ||||||||||||||||||||||||||||||
Db      99 ACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECN 158

Qy     121 STANTVCSSSVS 132
           ||||||||||||
Db     159 STANTVCSSSVS 170


RESULT 3
```

```
TNR6_PIG
ID   TNR6_PIG       STANDARD;      PRT;   332 AA.
AC   O77736;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001202; CAA04596.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    332       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 6.
FT   DOMAIN       17    175       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    176    192       POTENTIAL.
FT   DOMAIN      193    332       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       45     81       TNFR-CYS 1.
FT   REPEAT       82    125       TNFR-CYS 2.
FT   REPEAT      126    164       TNFR-CYS 3.
FT   DOMAIN      227    311       DEATH.
FT   DISULFID     46     57       BY SIMILARITY.
FT   DISULFID     58     71       BY SIMILARITY.
FT   DISULFID     61     80       BY SIMILARITY.
FT   DISULFID     83     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    141       BY SIMILARITY.
FT   DISULFID    144    155       BY SIMILARITY.
FT   DISULFID    147    163       BY SIMILARITY.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   332 AA;  37592 MW;  5B8B03682756BF1B CRC64;

  Query Match             26.4%;  Score 226.5;  DB 1;  Length 332;
  Best Local Similarity   29.9%;  Pred. No. 1.2e-12;
  Matches   43;  Conservative   28;  Mismatches   62;  Indels   11;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTC 68
           ||:|:::    ||: || |    | |  |    ||  |  |  :| |::    |  | |
Db      46 CPEGQHREGQFCCQPCPPGKRKHADCTSPGGAPQCVPCSEGEDYTDKNHHSSKCRRCRVC 105

Qy      69 DKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTV 126
           | :  :  :  |: | : || |:   :  :  :  | | ||| |  |  |:: |  |:||
Db     106 DGEHGLEVEKNCTRTQNTKCRCKPNFFCHTSQC-EHCNPCTTCEHG--VIENCTPTSNTK 162

Qy     127 C-----SSSVSNPRNWLFLLMLIV 145
           |     |:   :  :||: |::::
Db     163 CREVFQSAGSRSNLHWLWALLILI 186


RESULT 4
TNR6_BOVIN
ID   TNR6_BOVIN     STANDARD;      PRT;   323 AA.
AC   P51867;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96226401; PubMed=8634151;
RA   Yoo J., Stone R.T., Beattie C.W.;
RT   "Cloning and characterization of the bovine Fas.";
RL   DNA Cell Biol. 15:227-234(1996).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U34794; AAC48546.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
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DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    323       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 6.
FT   DOMAIN       17    170       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    171    188       POTENTIAL.
FT   DOMAIN      189    323       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       45     80       TNFR-CYS 1.
FT   REPEAT       81    124       TNFR-CYS 2.
FT   REPEAT      125    163       TNFR-CYS 3.
FT   DOMAIN      238    306       DEATH.
FT   DISULFID     45     56       BY SIMILARITY.
FT   DISULFID     57     70       BY SIMILARITY.
FT   DISULFID     60     79       BY SIMILARITY.
FT   DISULFID     82     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    140       BY SIMILARITY.
FT   DISULFID    143    154       BY SIMILARITY.
FT   DISULFID    146    162       BY SIMILARITY.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   323 AA;  36445 MW;  4D88A90E9E1F4892 CRC64;

  Query Match             25.6%;  Score 219.5;  DB 1;  Length 323;
  Best Local Similarity   31.4%;  Pred. No. 4.8e-12;
  Matches   44;  Conservative   26;  Mismatches   63;  Indels    7;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT-FTGKDNGLHDCELCST 67
             :| :| |: :  ||: || |      ||      :|  |  |  :| | :    |  ||
Db      44 SCQEGLYREHQFCCQPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTDKSHHSDKCIRCSI 103

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : || |:   :: :    | | ||| |  ||  :::|  |:||
Db     104 CDEEHGLEVEQNCTRTRNTKCRCKSN-FFCNSSPCEHCNPCTTCEHGI--IEKCTPTSNT 160

Qy     126 VCSSSVSNPRN-WLFLLMLI 144
           |  | |:  : |  |::||
Db     161 KCKGSRSHANSLWALLILLI 180


RESULT 5
TR1A_MOUSE
ID   TR1A_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Bebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   EMBL; BC004599; AAH04599.1; -.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
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DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    454       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    235       POTENTIAL.
FT   DOMAIN      236    454       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      339    349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      356    441       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    185    191       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    394    394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  0710C2E8C3C2B6D9 CRC64;

  Query Match             25.1%;  Score 215.5;  DB 1;  Length 454;
  Best Local Similarity   28.1%;  Pred. No. 1.4e-11;
  Matches   52;  Conservative   23;  Mismatches   61;  Indels   49;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :||  |  ||:: : |  |     | :|  ||||   | |  |  |
Db      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 103

Qy      67 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |: : |  : | |  |  | |    |   |  :  |   |  |: |  |  |  |
Db     104 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS--------------------------------SSVSNPRN-----WLFLLML 143
           | ||||:                                ::|:||::      | |::|
Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVIL 220

Qy     144 IVFCI 148
           :  |:
Db     221 LGLCL 225


RESULT 6
CRMB_COWPX
ID   CRMB_COWPX     STANDARD;      PRT;   351 AA.
AC   O73559;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90 / Grishak;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "The genomic sequence analysis of the left and right species-specific
RT   terminal region of a cowpox virus strain reveals unique sequences and
RT   a cluster of intact ORFs for immunomodulatory and host range
RT   proteins.";
RL   Virology 243:432-460(1998).
RN   [2]
RP   FUNCTION.
RC   STRAIN=Brighton red;
RX   PubMed=8091665;
RA   Hu F.Q., Smith C.A., Pickup D.J.;
RT   "Cowpox virus contains two copies of an early gene encoding a soluble
RT   secreted form of the type II TNF receptor.";
RL   Virology 204:343-356(1994).
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Y11842; CAA72578.1; -.
DR   EMBL; Y15035; CAA75306.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    351       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     67       TNFR-CYS 1.
FT   REPEAT       69    110       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     67       BY SIMILARITY.
FT   DISULFID     70     85       BY SIMILARITY.
FT   DISULFID     88    102       BY SIMILARITY.
FT   DISULFID     92    110       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   351 AA;  38253 MW;  57CAE73EF4E5D7C7 CRC64;

  Query Match             24.7%;  Score 211.5;  DB 1;  Length 351;
  Best Local Similarity   38.7%;  Pred. No. 2.5e-11;
  Matches   48;  Conservative   14;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-T 67
           | | ||  :::|| :|| ||:    |    :|  ||  |  |||| ::| |  |  |:
Db      32 CKDNEYNRHNLCCLSCPPGTYASRLCDSKTNTNTQCTPCGSGTFTSRNNHLPACLSCNGR 91

Qy      68 CDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN 124
           || :|     |: | :| |||  | ||   |    |: |   |||  |  |     || :
Db      92 CDSNQVETRSCNTTHNRICECAPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSTGD 149
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Qy     125 TVCS 128
           |||
Db     150 VVCS 153


RESULT 7
TR1A_RAT
ID   TR1A_RAT       STANDARD;      PRT;   461 AA.
AC   P22934; Q91V30; Q91Y93;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC   STRAIN=Various;
RA   Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT   among autoimmune susceptible and resistant inbred rat strains.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   EMBL; AF329976; AAK53562.1; -.
DR   EMBL; AF329977; AAK53563.1; -.
DR   EMBL; AF329981; AAK53567.1; -.
DR   EMBL; AF329978; AAK53564.1; -.
DR   EMBL; AF329979; AAK53565.1; -.
DR   EMBL; AF329980; AAK53566.1; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      363    448       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    195       BY SIMILARITY.
FT   DISULFID    185    191       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     230    230       I -> V (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                                 DA/BKL AND F344/NHSD).
FT   VARIANT     295    295       H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
FT                                 DA/BKL, F344/NHSD AND BN/SSNHSD).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FBD202 CRC64;

  Query Match             24.5%;  Score 210;  DB 1;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 4.1e-11;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   ::| :|| |  ||:: : |  |  :  || |  ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCK 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           || |:  |  :: | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     122 TANTVCS-------------------------------SSVSNPRN----------WL 138
            ||||:                               ::|:||::           :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     139 FLLMLIVFCI 148
           | :|   ||
Db     221 GLCLLFFICI 230


RESULT 8
CRMB_CAMPS
ID   CRMB_CAMPS     STANDARD;      PRT;   349 AA.
AC   Q8UYA7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
```

```
OS   Camelpox virus (strain CMS), and
OS   Camelpox virus (strain M-96).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=203172, 203173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMS;
RX   PubMed=11907336;
RA   Gubser C., Smith G.L.;
RT   "The sequence of camelpox virus shows it is most closely related to
RT   variola virus, the cause of smallpox.";
RL   J. Gen. Virol. 83:855-872(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M-96;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA   Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT   "The genome of camelpox virus.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY009089; AAG37456.1; -.
DR   EMBL; AY009089; AAG37718.1; -.
DR   EMBL; AF438165; AAL73920.1; -.
DR   EMBL; AF438165; AAL73917.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31     65       TNFR-CYS 1.
FT   REPEAT      67    108       TNFR-CYS 2.
FT   DISULFID    32     43       BY SIMILARITY.
FT   DISULFID    44     57       BY SIMILARITY.
FT   DISULFID    47     65       BY SIMILARITY.
FT   DISULFID    68     83       BY SIMILARITY.
FT   DISULFID    86    100       BY SIMILARITY.
FT   DISULFID    90    108       BY SIMILARITY.
FT   CARBOHYD   101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  38064 MW;  EA412AF991E087F3 CRC64;

  Query Match             24.3%;  Score 208.5;  DB 1;  Length 349;
  Best Local Similarity   37.4%;  Pred. No. 4.4e-11;
  Matches   46;  Conservative   15;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
           | | ||: :::|| :|| ||:    |    |  ||  |  |||| ::| |  |  |: |
Db      32 CKDNEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
           | :|     |: | :| |||  | ||   |    |: |   |||  |  |     |  :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCILKGSSGCKACVSQTKCGIGYGVSGH-TSAGDV 148

Qy     126 VCS 128
           :||
Db     149 ICS 151


RESULT 9
TNR6_MOUSE
ID   TNR6_MOUSE     STANDARD;      PRT;   327 AA.
AC   P25446; Q9DCQ1;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92148151; PubMed=1371136;
RA   Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
RA   Copeland N.G., Jenkins N.A., Nagata S.;
RT   "The cDNA structure, expression, and chromosomal assignment of the
RT   mouse Fas antigen.";
RL   J. Immunol. 148:1274-1279(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   Koczan D., Ibrahim S.M., Thiesen H.J.;
RT   "Role of a mutant fas receptor in a transgenic mouse.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE OF 1-96 FROM N.A.
RX   MEDLINE=93189576; PubMed=7680478;
RA   Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT   "Aberrant transcription caused by the insertion of an early
RT   transposable element in an intron of the Fas antigen gene of lpr
RT   mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN   [5]
RP   VARIANT LPR.
RX   MEDLINE=92195401; PubMed=1372394;
RA   Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA   Nagata S.;
RT   "Lymphoproliferation disorder in mice explained by defects in Fas
RT   antigen that mediates apoptosis.";
RL   Nature 356:314-317(1992).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
```

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CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC       LIVER, LUNG, HEART, AND ADULT OVARY.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC       DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC       PRODUCTION.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M83649; AAA37593.1; -.
DR   EMBL; AK002590; BAB22211.1; -.
DR   EMBL; AJ295702; CAC00638.1; -.
DR   EMBL; AJ295703; CAC00638.1; JOINED.
DR   EMBL; AJ295704; CAC00638.1; JOINED.
DR   EMBL; S56490; AAB25700.1; -.
DR   EMBL; S56485; AAB25700.1; JOINED.
DR   EMBL; S56486; AAB25700.1; JOINED.
DR   PIR; A46484; A46484.
DR   HSSP; P25445; 1DDF.
DR   MGD; MGI:95484; Tnfrsf6.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Disease mutation.
FT   SIGNAL        1     21
FT   CHAIN        22    327       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 6.
FT   DOMAIN       22    169       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    170    186       POTENTIAL.
FT   DOMAIN      187    327       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       43     79       TNFR-CYS 1.
FT   REPEAT       80    123       TNFR-CYS 2.
FT   REPEAT      124    162       TNFR-CYS 3.
FT   DOMAIN      222    306       DEATH.
FT   DISULFID     44     55       BY SIMILARITY.
FT   DISULFID     56     69       BY SIMILARITY.
FT   DISULFID     59     78       BY SIMILARITY.
FT   DISULFID     81     97       BY SIMILARITY.
FT   DISULFID    100    115       BY SIMILARITY.
FT   DISULFID    103    123       BY SIMILARITY.
FT   DISULFID    125    139       BY SIMILARITY.
FT   DISULFID    142    153       BY SIMILARITY.
FT   DISULFID    145    161       BY SIMILARITY.
FT   CARBOHYD     43     43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     246    246       I -> N (IN LPR).
FT   CONFLICT     38     38       H -> R (IN REF. 3).
SQ   SEQUENCE   327 AA;  37418 MW;  F6BFFC5ACE356EEE CRC64;
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  Query Match           23.9%;  Score 205;  DB 1;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 8.3e-11;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 67
           || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     126 VCSSSVSNPRNWLFLLMLIVFCI 148
           |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180


RESULT 10
CRMB_VARV
ID   CRMB_VARV      STANDARD;      PRT;   349 AA.
AC   P34015; Q89098; Q85407; Q89118;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   CRMB OR G2R OR G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=India-1967 / Isolate Ind3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bangladesh-1975;
RX   MEDLINE=94088747; PubMed=8264798;
RA   Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA   Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA   Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA   Venter C.J.;
RT   "Potential virulence determinants in terminal regions of variola
RT   smallpox virus genome.";
RL   Nature 366:748-751(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966, and Somalia-1977;
RA   Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA   Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966;
RX   MEDLINE=20107289; PubMed=10639322;
RA   Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA   Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA   Esposito J.J.;
RT   "Alastrim smallpox variola minor virus genome DNA sequences.";
RL   Virology 266:361-386(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
```

```
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   EMBL; L22579; AAA60933.1; -.
DR   EMBL; U18339; AAA69407.1; -.
DR   EMBL; U18341; AAA69467.1; -.
DR   EMBL; Y16780; CAB54798.1; -.
DR   EMBL; U88146; AAB94371.1; -.
DR   EMBL; U88148; AAB94373.1; -.
DR   EMBL; U88149; AAB94374.1; -.
DR   EMBL; U88152; AAB94377.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31     66       TNFR-CYS 1.
FT   REPEAT      67    108       TNFR-CYS 2.
FT   DISULFID    32     43       BY SIMILARITY.
FT   DISULFID    44     57       BY SIMILARITY.
FT   DISULFID    47     65       BY SIMILARITY.
FT   DISULFID    68     83       BY SIMILARITY.
FT   DISULFID    86    100       BY SIMILARITY.
FT   DISULFID    90    108       BY SIMILARITY.
FT   CARBOHYD   101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   215    215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     17     17       MISSING (IN STRAINS BANGLADESH-1975 AND
FT                               CHIMP 9-4).
FT   VARIANT    160    160       H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT                               1966 AND SOMALIA-1977).
FT   VARIANT    165    165       A -> T (IN STRAINS BUTLER-1952 AND
FT                               GARCIA-1966).
FT   VARIANT    182    182       E -> K (IN STRAIN SOMALIA-1977).
FT   VARIANT    274    274       A -> E (IN STRAIN SOMALIA-1977).
FT   VARIANT    335    335       N -> D (IN STRAINS BUTLER-1952 AND
FT                               GARCIA-1966).
FT   VARIANT    339    339       P -> L (IN STRAINS BUTLER-1952 AND
FT                               GARCIA-1966).
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;

  Query Match           23.4%;  Score 200.5;  DB 1;  Length 349;
  Best Local Similarity  36.6%;  Pred. No. 2.1e-10;
  Matches   45;  Conservative   16;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
           | | ||: :::|| :|| ||:    |    |  ||  |  |||| ::| |  |  |:  |
Db      32 CKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGRC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
           : :|     |: | :| |||  | ||   |    |: |   |||  |  |     |  :

Db      91 NSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGIGYGVSGH-TSVGDV 148

Qy     126 VCS 128
           :||
Db     149 ICS 151


RESULT 11
TR1A_HUMAN
ID   TR1A_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor
DE   binding protein 1 (TBPI)].
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90235285; PubMed=2158863;
RA   Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA   Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90235284; PubMed=2158862;
RA   Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA   Tabuchi H., Lesslauer W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE=91006021; PubMed=1698610;
RA   Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA   Aderka D., Holtmann H., Wallach D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91017509; PubMed=2170974;
RA   Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT   expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250049; PubMed=1315717;
RA   Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
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RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 41-45.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX   MEDLINE=93258809; PubMed=8387891;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE=97094982; PubMed=8939750;
RA   Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
RN   [11]
RP   VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX   MEDLINE=99213501; PubMed=10199409;
RA   McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,
RA   Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA   Pettersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA   Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
RA   Schlimgen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA   Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,
RA   Hitman G.A., O'Shea J., Kastner D.L.;
RT   "Germline mutations in the extracellular domains of the 55 kDa TNF
RT   receptor, TNFR1, define a family of dominantly inherited
RT   autoinflammatory syndromes.";
RL   Cell 97:133-144(1999).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis. Contributes to
CC       the induction of noncytocidal TNF effects including anti-viral
CC       state and activation of the acid sphingomyelinase.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- PTM: The soluble form is produced from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
CC       familial hibernian fever (FHF), a disease characterized by
CC       recurrent fever, abdominal pain, localized tender skin lesions and
CC       myalgia.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
DR   EMBL; M33294; AAA03210.1; -.
DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
DR   EMBL; A21522; CAA01558.1; -.
DR   EMBL; BC010140; AAH10140.1; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   Genew; HGNC:11916; TNFRSF1A.
DR   MIM; 191190; -.
DR   MIM; 142680; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Disease mutation; Polymorphism; 3D-structure.
FT   SIGNAL       1     21
FT   CHAIN       22    455       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1A, MEMBRANE FORM.
FT   CHAIN       41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    455       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     338    348       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356    441       DEATH.
FT   DISULFID    44     58
FT   DISULFID    59     72
FT   DISULFID    62     81
FT   DISULFID    84     99
FT   DISULFID   102    117
FT   DISULFID   105    125
FT   DISULFID   127    143
FT   DISULFID   146    158
FT   DISULFID   149    166
FT   DISULFID   168    179

  Query Match            23.4%;  Score 200.5;  DB 1;  Length 455;
  Best Local Similarity  33.6%;  Pred. No. 2.6e-10;
  Matches   42;  Conservative   16;  Mismatches   60;  Indels    7;  Gaps    4;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:| :|| |  ||::  | |     | :|  |:||  :| | |  ||
Db      44 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCS 103

Qy      67 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
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          | |:   |  : |:   |  | |:   | :|  :    |  |: | |  |   |
Db    104 KCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 162

Qy    124 NTVCS 128
          ||||:
Db    163 NTVCT 167


RESULT 12
TR1A_PIG
ID   TR1A_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=96011645; PubMed=7590278;
RA   Suter B., Pauli U.H.;
RT   "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT   receptor.";
RL   Gene 163:263-266(1995).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein..
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   ---------------------------------------------------------------------
DR   EMBL; U19994; AAC48499.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 1A.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     211   233       POTENTIAL.
FT   DOMAIN       234   461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT        43    82       TNFR-CYS 1.
FT   REPEAT        83   125       TNFR-CYS 2.
FT   REPEAT       126   166       TNFR-CYS 3.
FT   REPEAT       167   195       TNFR-CYS 4.
FT   DOMAIN       340   350       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN       362   447       DEATH.
FT   DISULFID      44    58       BY SIMILARITY.
FT   DISULFID      59    72       BY SIMILARITY.
FT   DISULFID      62    81       BY SIMILARITY.
FT   DISULFID      84    99       BY SIMILARITY.
FT   DISULFID     102   117       BY SIMILARITY.
FT   DISULFID     105   125       BY SIMILARITY.
FT   DISULFID     127   143       BY SIMILARITY.
FT   DISULFID     146   158       BY SIMILARITY.
FT   DISULFID     149   166       BY SIMILARITY.
FT   DISULFID     168   179       BY SIMILARITY.
FT   DISULFID     182   194       BY SIMILARITY.
FT   DISULFID     185   190       BY SIMILARITY.
FT   CARBOHYD      54    54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      86    86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     145   145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     151   151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50696 MW;  CD72361EC60C9D43 CRC64;

  Query Match             22.6%;  Score 193.5;  DB 1;  Length 461;
  Best Local Similarity   32.3%;  Pred. No. 1.1e-09;
  Matches   41;  Conservative   17;  Mismatches   58;  Indels   11;  Gaps    5;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
             || |:|   |:  :|| | ||::  | |    | :| |||  :| | | ||
Db      44 CPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCS 103

Qy      67 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 121
           |  : : |  : |:   | | |   |   |: : |   |  | |: || | |   |
Db     104 KCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLF--QCLNCSLCPNG-TVQLPCLE 160

Qy     122 TANTVCS 128
             :|:|:
Db     161 KQDTICN 167


RESULT 13
TNR6_RAT
ID   TNR6_RAT       STANDARD;      PRT;   324 AA.
AC   Q63199;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR PT1 OR FAS.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=94128114; PubMed=7507668;
RA   Kimura K., Yamamoto M., Wakatsuki T.;
RT   "A variant mRNA species encoding a truncated form of Fas antigen in
RT   the rat liver.";
RL   Biochem. Biophys. Res. Commun. 198:666-674(1994).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
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CC       both (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D26112; BAA05108.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL       1    21       BY SIMILARITY.
FT   CHAIN       22   324       TUMOR NECROSIS FACTOR RECEPTOR
FT                              SUPERFAMILY MEMBER 6.
FT   DOMAIN      22   171       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   172   188       POTENTIAL.
FT   DOMAIN     189   324       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43    79       TNFR-CYS 1.
FT   REPEAT      80   123       TNFR-CYS 2.
FT   REPEAT     124   163       TNFR-CYS 3.
FT   DOMAIN     219   303       DEATH.
FT   DISULFID    44    55       BY SIMILARITY.
FT   DISULFID    56    69       BY SIMILARITY.
FT   DISULFID    59    78       BY SIMILARITY.
FT   DISULFID    81    97       BY SIMILARITY.
FT   DISULFID   100   115       BY SIMILARITY.
FT   DISULFID   103   123       BY SIMILARITY.
FT   DISULFID   125   139       BY SIMILARITY.
FT   DISULFID   142   154       BY SIMILARITY.
FT   DISULFID   145   162       BY SIMILARITY.
FT   CARBOHYD    43    43       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   114   114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   132   132       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   324 AA;  36835 MW;  D25D583C909D9D09 CRC64;

  Query Match             22.1%;  Score 190;  DB 1;  Length 324;
  Best Local Similarity   30.7%;  Pred. No. 1.6e-09;
  Matches   46;  Conservative   22;  Mismatches   64;  Indels   18;  Gaps    8;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT----FTGKDNGLHDCEL 64
           || :| ||    ||: |  |       |    | |    ||| |    :| : :    |
Db      43 NCSEGLYQVGPFCCQPCQPGERKVKDCT---TSGGAPTCHPCTEGEEYTDRKHYSDKCRR 99

Qy      65 CSTCDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGI-PVLQECNS 121
           |: ||:   :  :  |: | : || |:   :| :    : |  || |  |:  :|: |
Db     100 CAFCDEGHGLEVETNCTRTQNTKCRCKEN-FYCNASLCDHCYHCTSC--GLEDILEPCTR 156

Qy     122 TANTVCSSSVSNPR-NWLFLL----MLIVF 146
           |:|| |    || :  || :|    :| ||
Db     157 TSNTKCKKQSSNYKLLWLLILPGLAILFVF 186


RESULT 14
TNR6_HUMAN
ID   TNR6_HUMAN     STANDARD;      PRT;   335 AA.
AC   P25445; Q14293; Q14294; Q14295; Q14292; Q16652;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE   receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE   (CD95).
GN   TNFRSF6 OR APT1 OR FAS OR FAS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91309137; PubMed=1713127;
RA   Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA   Sameshima M., Hase A., Seto Y., Nagata S.;
RT   "The polypeptide encoded by the cDNA for human cell surface antigen
RT   Fas can mediate apoptosis.";
RL   Cell 66:233-243(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
RP   321-335.
RX   MEDLINE=92268122; PubMed=1375228;
RA   Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA   Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA   Krammer P.H.;
RT   "Purification and molecular cloning of the APO-1 cell surface
RT   antigen, a member of the tumor necrosis factor/nerve growth factor
RT   receptor superfamily. Sequence identity with the Fas antigen.";
RL   J. Biol. Chem. 267:10709-10715(1992).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
RX   MEDLINE=95181785; PubMed=7533181;
RA   Cascino I., Fiucci G., Papoff G., Ruberti G.;
RT   "Three functional soluble forms of the human apoptosis-inducing Fas
RT   molecule are produced by alternative splicing.";
RL   J. Immunol. 154:2706-2713(1995).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 5).
RC   TISSUE=Peripheral blood lymphocytes;
RA   Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RX   MEDLINE=96238926; PubMed=8648105;
RA   Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;
RT   "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants
RT   prevents cell death in vitro.";
RL   J. Immunol. 156:4622-4630(1996).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Urinary bladder;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   STRUCTURE BY NMR OF 218-335.
RX   MEDLINE=97122332; PubMed=8967952;
RA   Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT   "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL   Nature 384:638-641(1996).
RN   [8]
RP   VARIANT ALPS PRO-241.
RX   MEDLINE=95300225; PubMed=7540117;
RA   Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
RA   Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;
RT   "Dominant interfering Fas gene mutations impair apoptosis in a human
RT   autoimmune lymphoproliferative syndrome.";
RL   Cell 81:935-946(1995).
RN   [9]
RP   VARIANT ALPS TYR-260.
RX   MEDLINE=97066823; PubMed=8929361;
RA   Drappa J., Vaishnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
RT   "Fas gene mutations in the Canale-Smith syndrome, an inherited
RT   lymphoproliferative disorder associated with autoimmunity.";
```

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RL   New Engl. J. Med. 335:1643-1649(1996).
RN   [10]
RP   VARIANTS ALPS TRP-121 AND CYS-232.
RX   MEDLINE=97180145; PubMed=9028321;
RA   Bettinardi A., Brugnoni D., Quiros-Roldan E., Malagoli A.,
RA   La Grutta S., Correra A., Notarangelo L.D.;
RT   "Missense mutations in the Fas gene resulting in autoimmune
RT   lymphoproliferative syndrome: a molecular and immunological
RT   analysis.";
RL   Blood 89:902-909(1997).
RN   [11]
RP   VARIANTS ALPS ASP-257 AND SER-310.
RX   MEDLINE=97180739; PubMed=9028957;
RA   Sneller M.C., Wang J., Dale J.K., Strober W., Middelton L.A., Choi Y.,
RA   Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
RA   Straus S.E.;
RT   "Clincial, immunologic, and genetic features of an autoimmune
RT   lymphoproliferative syndrome associated with abnormal lymphocyte
RT   apoptosis.";
RL   Blood 89:1341-1348(1997).
RN   [12]
RP   VARIANT ALPS ALA-28.
RX   MEDLINE=97463833; PubMed=9322534;
RA   Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
RA   Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
RA   Levrero M.;
RT   "Fas/Apol mutations and autoimmune lymphoproliferative syndrome in a
RT   patient with type 2 autoimmune hepatitis.";
RL   Gastroenterology 113:1384-1389(1997).
RN   [13]
RP   VARIANT ALPS VAL-260.
RX   MEDLINE=99038860; PubMed=9821419;
RA   Infante A.J., Britton H.A., DeNapoli T., Middelton L.A., Lenardo M.J.,
RA   Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;
RT   "The clinical spectrum in a large kindred with autoimmune
RT   lymphoproliferative syndrome caused by a Fas mutation that impairs
RT   lymphocyte apoptosis.";
RL   J. Pediatr. 133:629-633(1998).
RN   [14]
RP   VARIANTS ALPS LYS-241 AND GLN-250.
RX   MEDLINE=99192346; PubMed=10090885;
RA   Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
RA   Dale J.K., Fleisher T.A., Middelton L.A., Sneller M.C., Lenardo M.J.,
RA   Straus S.E., Puck J.M.;
RT   "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
RT   influences penetrance.";
RL   Am. J. Hum. Genet. 64:1002-1014(1999).
RN   [15]
RP   VARIANT ALPS GLY-272.
RX   MEDLINE=99270228; PubMed=10340403;
RA   Peters A.M., Kohfink B., Martin H., Griesinger F., Wormann B.,
RA   Gahr M., Roesler J.;
RT   "Defective apoptosis due to a point mutation in the death domain of
RT   CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
RT   lymphoma, and Hodgkin's disease.";
RL   Exp. Hematol. 27:868-874(1999).
RN   [16]
RP   VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
RX   MEDLINE=99126461; PubMed=9927496;
RA   Vaishnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,
RA   Elkon K.B.;
RT   "The molecular basis for apoptotic defects in patients with CD95
RT   (Fas/Apo-1) mutations.";
RL   J. Clin. Invest. 103:355-363(1999).
RN   [17]
RP   VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
RP   VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
RX   MEDLINE=99005325; PubMed=9787134;
RA   Groenbaek K., Straten P.T., Ralfkiaer E., Ahrenkiel V., Andersen M.K.,
RA   Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
RT   "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
RT   extranodal disease and autoimmunity.";
RL   Blood 92:3018-3024(1998).
RN   [18]
RP   VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
RX   MEDLINE=21311411; PubMed=11418480;
RA   Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
RA   Roesen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
RA   Fischer R.E., Jackson C.M., Lin A.Y., Baeumler C., Siegert E.,
RA   Marx A., Vaishnaw A.K., Grodzicky T., Fleisher T.A., Lenardo M.J.;
RT   "The development of lymphomas in families with autoimmune
RT   lymphoproliferative syndrome with germline Fas mutations and
RT   defective lymphocyte apoptosis.";
RL   Blood 98:194-200(2001).
CC   -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC       recruits caspase-8 to the activated receptor. The resulting death-
CC       inducing signaling complex (DISC) performs caspase-8 proteolytic
CC       activation which initiates the subsequent cascade of caspases
CC       (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC       mediated apoptosis may have a role in the induction of peripheral
CC       tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC       both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC       Secreted (isoforms 2 to 6).
CC   -!- ALTERNATIVE PRODUCTS: 6 isoforms; 1 (shown here), 2/Del2/d,
CC       3/Del3/e, 4/b, 5/c and 6/TMDel/a; are produced by alternative
CC       splicing.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
CC       lymphoproliferative syndrome (ALPS), also known as Canale-Smith
CC       syndrome (CSS), a childhood syndrome involving hemolytic anemia
CC       and thrombocytopenia with massive lymphadenopathy and
CC       splenomegaly.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M67454; AAA63174.1; -.
DR   EMBL; X63717; CAA45250.1; -.
DR   EMBL; X89101; CAA61473.1; -.
DR   EMBL; Z47993; CAA88031.1; -.
DR   EMBL; Z47994; CAA88032.1; -.
DR   EMBL; Z47995; CAA88033.1; -.
DR   EMBL; Z70520; CAA94431.1; -.

  Query Match             22.1%;  Score 189.5;  DB 1;  Length 335;
  Best Local Similarity   30.9%;  Pred. No. 1.8e-09;
  Matches   42;  Conservative   19;  Mismatches   68;  Indels    7;  Gaps    5;

Qy      12 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 70
           :| :     | | || |      | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109

Qy      71 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 128
              :  :  |: | : || |:   :: :    | | |||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     129 SSVSNPR-NWLFLLML 143
             |     || ||:|
Db     167 EEGSRSNLGWLCLLLL 182


RESULT 15
TR1A_BOVIN
ID   TR1A_BOVIN     STANDARD;      PRT;   471 AA.
AC   O19131;
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DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE   (TNF-R1) (TNF-RI) (p55).
GN   TNFRSF1A OR TNFR1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98273505; PubMed=9613449;
RA   Lee E.-K., Kehrli M.E. Jr., Taylor M.J.;
RT   "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
RT   (TNF)-receptor I.";
RL   Vet. Immunol. Immunopathol. 61:379-385(1998).
CC   -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC       caspase-8 to the activated receptor. The resulting death-inducing
CC       signaling complex (DISC) performs caspase-8 proteolytic activation
CC       which initiates the subsequent cascade of caspases (aspartate-
CC       specific cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U90937; AAB65143.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   Pfam; PF00531; death; 1.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    471       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1A.
FT   DOMAIN      22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211    233       POTENTIAL.
FT   DOMAIN     234    471       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    195       TNFR-CYS 4.
FT   DOMAIN     340    360       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     372    457       DEATH.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    194       BY SIMILARITY.
FT   DISULFID   185    190       BY SIMILARITY.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   471 AA;  51367 MW;  5243EF514DFE81C4 CRC64;

  Query Match             21.7%;  Score 186.5;  DB 1;  Length 471;
  Best Local Similarity   32.6%;  Pred. No. 4.2e-09;
  Matches   42;  Conservative   16;  Mismatches   54;  Indels   17;  Gaps    6;

Qy      10 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 66
           || |:|   |:: :|| |  ||::   |  |     |  | |||:|  :| |  |  ||
Db      44 CPQGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRRCLSCS 103

Qy      67 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQG---IPVLQE 118
             |  :  |  :: |    |  | |   |   |: :  |   |  |: || |   ||
Db     104 RCRDEMFQVEISPCVVDRDTVCGCRKNQYREYWGETGF--RCLNCSLCPNGTVNIP---- 157

Qy     119 CNSTANTVC 127
           |    :|:|
Db     158 CQERQDTIC 166


Search completed: December 10, 2002, 15:06:17
Job time : 9.30864 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:03:51 ; Search time 24.2099 Seconds
(without alignments)
1259.609 Million cell updates/sec

Title: US-09-855-266A-2
Perfect score: 858
Sequence: 1 AMPESYSFNCPDGEYQSNDV.....SSVSNPRNWLFLLMLIVFCI 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	288.5	33.6	438	13	Q9DFV0	Q9dfv0 brachydanio
2	246.5	28.7	357	13	Q9DF34	Q9df34 brachydanio
3	220.5	25.7	327	6	O97491	O97491 ovis aries
4	218.5	25.5	263	6	Q9XS60	Q9xs60 oryctolagus
5	218.5	25.5	320	6	Q9XS29	Q9xs29 oryctolagus
6	217.5	25.3	189	6	Q95185	Q95185 felis silve
7	217.5	25.3	319	6	Q9TV79	Q9tv79 oryctolagus
8	215.5	25.1	446	6	Q95ND3	Q95nd3 felis silve
9	214.5	25.0	347	12	O57119	O57119 cowpox viru
10	214.5	25.0	351	12	O57121	O57121 cowpox viru
11	211.5	24.7	348	12	O57103	O57103 monkeypox v
12	211.5	24.7	348	12	O57108	O57108 monkeypox v
13	211.5	24.7	348	12	O57277	O57277 monkeypox v
14	211.5	24.7	349	12	O57101	O57101 monkeypox v
15	211.5	24.7	349	12	O57102	O57102 monkeypox v
16	211.5	24.7	349	12	O57291	O57291 monkeypox v
17	211.5	24.7	351	12	O73559	O73559 cowpox viru
18	209.5	24.4	326	12	O57120	O57120 cowpox viru
19	209.5	24.4	360	12	O57118	O57118 cowpox viru
20	208.5	24.3	349	12	O57098	O57098 camelpox vi
21	208.5	24.3	349	12	O57099	O57099 monkeypox v
22	208.5	24.3	349	12	Q8UYA7	Q8uya7 camelpox vi
23	208.5	24.3	349	12	O57284	O57284 camelpox vi
24	207.5	24.2	189	6	O97530	O97530 canis famil
25	207.5	24.2	326	12	O57122	O57122 cowpox viru
26	207.5	24.2	351	12	O57117	O57117 cowpox viru
27	205.5	24.0	349	12	O57100	O57100 monkeypox v
28	205.5	24.0	349	12	O57109	O57109 variola vir
29	204.5	23.8	347	12	O57115	O57115 cowpox viru
30	204.5	23.8	349	12	O57305	O57305 cowpox viru
31	202.5	23.6	349	12	O57097	O57097 camelpox vi
32	200.5	23.4	348	12	O57112	O57112 variola vir
33	200.5	23.4	348	12	Q85407	Q85407 variola vir
34	200.5	23.4	349	12	O57110	O57110 variola vir
35	200.5	23.4	349	12	O57111	O57111 variola vir
36	200.5	23.4	349	12	Q89098	Q89098 variola vir
37	200.5	23.4	349	12	Q89118	Q89118 variola vir
38	197.5	23.0	355	12	Q85308	Q85308 cowpox viru
39	195.5	22.8	350	12	O57123	O57123 cowpox viru
40	190.5	22.2	331	6	Q9TSN4	Q9tsn4 macaca fasc
41	190.5	22.2	331	6	Q9BDN0	Q9bdn0 macaca neme
42	190.5	22.2	350	12	O57116	O57116 cowpox viru
43	190	22.1	186	12	O72735	O72735 cowpox viru
44	190	22.1	186	12	Q911R5	Q911r5 vaccinia vi
45	189.5	22.1	331	6	Q9BDN4	Q9bdn4 cercocebus

ALIGNMENTS

RESULT 1
Q9DFV0
ID Q9DFV0 PRELIMINARY; PRT; 438 AA.
AC Q9DFV0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ovarian TNF receptor.
GN TNFRSFA.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250042; AAG24365.1; -.
DR HSSP; O14763; 1D0G.
DR ZFIN; ZDB-GENE-010802-1; tnfrsfa.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;

Query Match 33.6%; Score 288.5; DB 13; Length 438;
Best Local Similarity 35.1%; Pred. No. 1.5e-24;

```
  Matches   53;  Conservative   22;  Mismatches   59;  Indels   17;  Gaps    2;

Qy      14 EYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQN 73
           ||  |  ||| | :||:||  |   |  |:|  |  ||:     |:  |  || | :||
Db      49 EYPHNGFCCKNCEAGTYVKEKCTSGHVMGKCSPCEKGTYAEHPTGMEQCLQCSQCHRDQT 108

Qy      74 MVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC------ 127
           :||:|::||: ||:|: | :    :  | |: ||||      :  |  |:|| |
Db     109 VVAECTSTSNTKCDCKFGTFCLPDEPCEVCKKCTKCKADEEEVSGCTPTSNTKCRRRPSY 168

Qy     128 -------SSSVSNPRNWLF----LLMLIVFC 147
                 | ||    :|    :|:|:| |
Db     169 PTEGPTEKPSASNSTGTIFVIVSILILLVIC 199


RESULT 2
Q9DF34
ID   Q9DF34      PRELIMINARY;      PRT;   357 AA.
AC   Q9DF34;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Death receptor.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT   "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
RT   receptor in transgenic zebrafish.";
RL   Nat. Cell Biol. 0:0-0(2000).
DR   EMBL; AF302789; AAG21396.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   357 AA;  40662 MW;  1652B4840D9EEDBA CRC64;

  Query Match             28.7%;  Score 246.5;  DB 13;  Length 357;
  Best Local Similarity   31.1%;  Pred. No. 7.1e-20;
  Matches   47;  Conservative   30;  Mismatches   67;  Indels    7;  Gaps    3;

Qy       5 SYSFNCPDG-EYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCE 63
           |   :| :| ||   ::||  ||:||:||  |     :| |  |   |:|  |:||  |
Db      36 SRDVSCREGLEYPHENICCLNCPAGTYVKKACAAAAEKGVCAPCEFDTYTEHDHGLLKCI 95

Qy      64 LCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTA 123
            |  |  ||  :  |::| : :|:|: | :    :  | |: |::| :     : | : :
Db      96 SCDKCRIDQETIEKCTSTQNTRCKCRNGSFCLPDQACEVCKKCSRCKEDEETEKSCTAIS 155

Qy     124 NTVC----SSSVSNPRNWLFLLMLIVF--CI 148
           ||||    |  |    :: :: |||   |:
Db     156 NTVCRKRNSPGSSTSMTFIVIMPLIVLLACV 186


RESULT 3
O97491
ID   O97491      PRELIMINARY;      PRT;   327 AA.
AC   O97491;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Fas protein.
GN   FAS.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPHOCYTE;
RA   Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT   "Cloning of sheep fas antigen.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB011671; BAA37093.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   327 AA;  36928 MW;  5CFEE844B2BE387A CRC64;

  Query Match             25.7%;  Score 220.5;  DB 6;  Length 327;
  Best Local Similarity   30.6%;  Pred. No. 5.9e-17;
  Matches   44;  Conservative   28;  Mismatches   65;  Indels    7;  Gaps    5;

Qy       9 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGT-FTGKDNGLHDCELCST 67
           :| :| |: :  ||: || |      ||      :|  |  |  :| | :    |  ||
Db      46 SCQEGLYREHLFCCQPCPPGKRKNGDCKRDGDMPECVLCSEGNEYTDKSHHSDKCIRCSV 105

Qy      68 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 125
           ||::  :  :  |: | : || |:   :: :    | | ||| |  ||  :::|  |:||
Db     106 CDEEHGLEVEHNCTRTQNTKCRCKSN-FFCNSSPCEHCNPCTTCEHGI--IEKCTPTSNT 162

Qy     126 VCSSSVSNPRN-WLFLLMLIVFCI 148
           |  | |:  : |  |::|::  |
Db     163 KCKGSRSHTNSLWALLILLLLILI 186


RESULT 4
Q9XS60
ID   Q9XS60      PRELIMINARY;      PRT;   263 AA.
AC   Q9XS60;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fas antigen spliced variant.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021297; BAA78429.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   263 AA;  30374 MW;  6D76782ADED1BFD7 CRC64;

  Query Match             25.5%;  Score 218.5;  DB 6;  Length 263;
  Best Local Similarity   33.1%;  Pred. No. 7.9e-17;
  Matches   46;  Conservative   19;  Mismatches   63;  Indels   11;  Gaps    5;

Qy      15 YQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQN 73
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          | | : ||: || ||  || |     :  || |  |  :| | :    |  || || :
Db     38 YLSGNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHG 97

Qy     74 M--VADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSV 131
          :    ||:   : || |:   :    |  | | ||| |  ||  ::||  |:|| |
Db     98 LEVETDCTTIQNTKCRCKSNFFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKG 154

Qy    132 SNPRN-----WLFLLMLIV 145
          |   :     ||  ::|::
Db    155 STTGSKHHFLWLLCILLLI 173


RESULT 5
Q9XS29
ID   Q9XS29      PRELIMINARY;      PRT;   320 AA.
AC   Q9XS29;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   C-type FAS antigen.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021299; BAA78431.1; -.
DR   EMBL; AB021296; BAA78428.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   320 AA;  36102 MW;  DA235E243220FFB3 CRC64;

  Query Match           25.5%;  Score 218.5;  DB 6;  Length 320;
  Best Local Similarity   33.1%;  Pred. No. 9.7e-17;
  Matches   46;  Conservative   19;  Mismatches   63;  Indels   11;  Gaps    5;

Qy     15 YQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQN 73
          | | : ||: || ||  || |     :  || |  |  :| | :    |  || || :
Db     38 YLSGNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHG 97

Qy     74 M--VADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSV 131
          :    ||:   : || |:   :    |  | | ||| |  ||  ::||  |:|| |
Db     98 LEVETDCTTIQNTKCRCKSNFFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKG 154

Qy    132 SNPRN-----WLFLLMLIV 145
          |   :     ||  ::|::
Db    155 STTGSKHHFLWLLCILLLI 173


RESULT 6
Q95185
ID   Q95185      PRELIMINARY;      PRT;   189 AA.
AC   Q95185;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumour necrosis factor receptor p60 (Fragment).
GN   TNFR-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Duthie S., Nasir L., Eckersall P.D.;
RT   "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT   partial cds.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U72344; AAB95089.1; -.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER     189    189
SQ   SEQUENCE   189 AA;  21420 MW;  F3FBE0CE809D7DBE CRC64;

  Query Match           25.3%;  Score 217.5;  DB 6;  Length 189;
  Best Local Similarity   35.1%;  Pred. No. 7.4e-17;
  Matches   46;  Conservative   16;  Mismatches   62;  Indels    7;  Gaps    4;

Qy      4 ESYSFNCPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
          |  :  || |:|   | | :||  |  ||::   |: |     | :|  ||||  :| |
Db     38 EKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDCEGPGLDTDCRECENGTFTASENYLR 97

Qy     61 DCELCSTCDKD--QNMVADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQ 117
          |  || | |:  |  :: |:   |  | |:   | ||  :    |  |: |  |  |
Db     98 QCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNG-TVQI 156

Qy    118 ECNSTANTVCS 128
          |  | ||||:
Db    157 SCKETQNTVCT 167


RESULT 7
Q9TV79
ID   Q9TV79      PRELIMINARY;      PRT;   319 AA.
AC   Q9TV79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   B-type Fas antigen.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isono T., Tanbe Y., Nagano Y., Seto A.;
RT   "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021298; BAA78430.1; -.
DR   HSSP; P25445; 1DDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   319 AA;  35961 MW;  06FA0033B1846591 CRC64;

  Query Match           25.3%;  Score 217.5;  DB 6;  Length 319;
  Best Local Similarity   34.8%;  Pred. No. 1.3e-16;
  Matches   48;  Conservative   16;  Mismatches   63;  Indels   11;  Gaps    5;

Qy     15 YQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDKDQN 73
          | | : ||: || ||  || |     :  || |  |  :| | :    |  || || :
Db     38 YLSGNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHG 97
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Qy      74 M--VADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSV 131
           :    ||:   : || |:   :    |  | | ||| |  ||  ::||  |:|| |
Db      98 LEVETDCTTIQNTKCRCKSNFFCNALKC-EHCDPCTMCEHGI--IEECTQTSNTKCKEKG 154

Qy     132 SNPRN-----WLFLLMLI 144
           |   :     ||  |:||
Db     155 STTGSKHHLFWLSTLLLI 172


RESULT 8
Q95ND3
ID   Q95ND3      PRELIMINARY;      PRT;   446 AA.
AC   Q95ND3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Tumor necrosis factor type I.
GN   TNFR I.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT   "Molecular cloning of feline tumor necrosis factor receptor type I
RT   (TNFR I ) and expression of TNFR I and TNFR II in various disease in
RT   cats.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB051103; BAB55455.1; -.
DR   InterPro; IPR000345; CytC_heme_bind.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   446 AA;  49563 MW;  217BD331DD8A74AA CRC64;

  Query Match             25.1%;  Score 215.5;  DB 6;  Length 446;
  Best Local Similarity   35.1%;  Pred. No. 3e-16;
  Matches   46;  Conservative   15;  Mismatches   63;  Indels    7;  Gaps    4;

Qy       4 ESYSFNCPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
           |  :  || |:|   | | :||  |  ||::   |  |     | :|  ||||  :| |
Db      38 EKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDCAGPGLDTDCRECENGTFTASENYLR 97

Qy      61 DCELCSTCDKD--QNMVADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQ 117
             |  || | |:  |  :: |:   |  | |:   | ||  :    |  |: |  |  |
Db      98 QCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQYRYYWSETHFQCLNCSLCLNG-TVQI 156

Qy     118 ECNSTANTVCS 128
           |  | ||||:
Db     157 SCKETQNTVCT 167


RESULT 9
O57119
ID   O57119      PRELIMINARY;      PRT;   347 AA.
AC   O57119;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH EP2-1975(ELEPHANT);
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90230; AAB94386.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   347 AA;  37971 MW;  A51B36A5619F48DA CRC64;

  Query Match             25.0%;  Score 214.5;  DB 12;  Length 347;
  Best Local Similarity   37.9%;  Pred. No. 3e-16;
  Matches   47;  Conservative   15;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-T 67
           | | ||: : :|| :|| ||:    |    :|  ||  |  |||| ::| |  |  |:
Db      29 CKDNEYKHHHLCCLSCPPGTYASRLCDSKTNTNTQCTSCGSGTFTSRNNHLPACLSCNGR 88

Qy      68 CDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN 124
           || :|     |: | :| |||  | ||   |    |: |   |||  |  |     || :
Db      89 CDSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGMGYGVSGH-TSTGD 146

Qy     125 TVCS 128
             :||
Db     147 VICS 150


RESULT 10
O57121
ID   O57121      PRELIMINARY;      PRT;   351 AA.
AC   O57121;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH OPV89/4(CAT);
RX   MEDLINE=20579014; PubMed=11136755;
RA   Loparev V.N., Massung R.F., Esposito J.J., Meyer H.;
RT   "Detection and differentiation of old world orthopoxviruses:
RT   restriction fragment length polymorphism of the crmB gene region.";
RL   J. Clin. Microbiol. 39:94-100(2001).
DR   EMBL; U90232; AAB94388.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   351 AA;  38394 MW;  6D0E4040C0EFEF78 CRC64;

  Query Match             25.0%;  Score 214.5;  DB 12;  Length 351;
  Best Local Similarity   37.9%;  Pred. No. 3e-16;
  Matches   47;  Conservative   15;  Mismatches   55;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-T 67
```

```
          | | ||: : :|| :|| ||:    |    :|  ||  |  |||| ::| |  |  |:
Db     32 CKDNEYKHHHLCCLSCPPGTYASRLCDSKTNTNTQCTSCGSGTFTSRNNHLPACLSCNGR 91

Qy     68 CDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN 124
          || :|     |: | :| ||| | ||   |    |: |   ||| |  |     || :
Db     92 CDSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCKACVSQTKCGMGYGVSGH-TSTGD 149

Qy    125 TVCS 128
           :||
Db    150 VICS 153


RESULT 11
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;

  Query Match             24.7%;  Score 211.5;  DB 12;  Length 348;
  Best Local Similarity   39.0%;  Pred. No. 6.6e-16;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy     10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
          | | ||:| ::|| :|| ||:    |    |  ||  |   |||  :| |  |  |:  |
Db     32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy     69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
          | :|     |: | :| ||| | ||   |    || |   |||  |  |     || :
Db     91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy    126 VCS 128
           :||
Db    149 ICS 151


RESULT 12
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;

  Query Match             24.7%;  Score 211.5;  DB 12;  Length 348;
  Best Local Similarity   39.0%;  Pred. No. 6.6e-16;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy     10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
          | | ||:| ::|| :|| ||:    |    |  ||  |   |||  :| |  |  |:  |
Db     32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy     69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
          | :|     |: | :| ||| | ||   |    || |   |||  |  |     || :
Db     91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy    126 VCS 128
           :||
Db    149 ICS 151


RESULT 13
O57277
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog (J2R) (J2L).
GN   CRMB OR J2R OR J2L.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RX   MEDLINE=21592287; PubMed=11734207;
RA   Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
RA   Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA   Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA   Sandakhchiev L.S.;
RT   "Human monkeypox and smallpox viruses: genomic comparison.";
RL   FEBS Lett. 509:66-70(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RA   Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
RA   Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA   Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   EMBL; AF380138; AAL40648.1; -.
DR   EMBL; AF380138; AAL40460.1; -.
DR   HSSP; O14763; 1D0G.
```

```
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  54019521556C2D8F CRC64;

  Query Match             24.7%;  Score 211.5;  DB 12;  Length 348;
  Best Local Similarity   39.0%;  Pred. No. 6.6e-16;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
           | | ||:| ::|| :|| ||:    |    | ||  |   ||| :| |  |  |:  |
Db      32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
           | :|     |: | :| |||  | ||   |    || |   |||  | |     || :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy     126 VCS 128
           :||
Db     149 ICS 151


RESULT 14
O57101
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38311 MW;  02F65B00CFB858BE CRC64;

  Query Match             24.7%;  Score 211.5;  DB 12;  Length 349;
  Best Local Similarity   39.0%;  Pred. No. 6.6e-16;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
           | | ||:| ::|| :|| ||:    |    | ||  |   ||| :| |  |  |:  |
Db      32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
           | :|     |: | :| |||  | ||   |    || |   |||  | |     || :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy     126 VCS 128
           :||
Db     149 ICS 151


RESULT 15
O57102
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BENIN-1978;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38308 MW;  CBD2C949F994C59C CRC64;

  Query Match             24.7%;  Score 211.5;  DB 12;  Length 349;
  Best Local Similarity   39.0%;  Pred. No. 6.6e-16;
  Matches   48;  Conservative   12;  Mismatches   56;  Indels    7;  Gaps    5;

Qy      10 CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS-TC 68
           | | ||:| ::|| :|| ||:    |    | ||  |   ||| :| |  |  |:  |
Db      32 CKDNEYRSRNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSDTFTSHNNHLQACLSCNGRC 90

Qy      69 DKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTANT 125
           | :|     |: | :| |||  | ||   |    || |   |||  | |     || :
Db      91 DSNQVETRSCNTTHNRICECSPG-YYCLLKGASGCRTCISKTKCGIGYGV-SGYTSTGDV 148

Qy     126 VCS 128
           :||
Db     149 ICS 151


Search completed: December 10, 2002, 15:07:16
Job time : 25.2099 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 14:56:26 ; Search time 34.7654 Seconds
(without alignments)
674.581 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1000	100.0	176	19	AAW80254	Amino acid sequenc
2	350.5	35.0	380	22	ABG09344	Novel human diagno
3	280	28.0	204	23	ABB81467	Murine TACH protei
4	209	20.9	461	11	AAR07450	Rat Tumour Necrosi
5	206.5	20.6	355	16	AAR85073	Cowpox virus T2-eq
6	206.5	20.6	355	22	AAB50524	Human tumour necro
7	206.5	20.6	455	11	AAR07451	Human Tumour Necro
8	205.5	20.5	168	13	AAR24084	Truncated TNF-alph
9	205.5	20.5	199	13	AAR24080	Truncated TNF-alph
10	205.5	20.5	211	20	AAW89225	Tumour necrosis fa
11	205.5	20.5	280	22	AAB66979	Tnfrl protein. Un
12	205.5	20.5	311	20	AAW89229	Tumour necrosis fa
13	205.5	20.5	366	20	AAW89228	Tumour necrosis fa
14	205.5	20.5	371	11	AAR07449	Tumour Necrosis Fa
15	205.5	20.5	397	20	AAW89227	Tumour necrosis fa
16	205.5	20.5	417	20	AAW89226	Tumour necrosis fa
17	205.5	20.5	420	20	AAW89224	Tumour necrosis fa
18	205.5	20.5	455	12	AAR10986	30kD TNF inhibitor
19	205.5	20.5	455	12	AAR11082	Human 55kD TNF-bin
20	205.5	20.5	455	13	AAR24000	TNF-alpha 55kD rec
21	205.5	20.5	455	14	AAR42059	Lambda derived TNF
22	205.5	20.5	455	16	AAR75084	p55 TNF-R. Homo s
23	205.5	20.5	455	20	AAY30934	Human tumour necro
24	205.5	20.5	455	21	AAB36266	Human tumour necro
25	205.5	20.5	455	21	AAB37800	Human tumour necro
26	205.5	20.5	455	21	AAB26984	Human TNFR 1. Hom
27	205.5	20.5	455	21	AAB23446	Human tumour necro
28	205.5	20.5	455	21	AAB01336	TNF-Rl death recep
29	205.5	20.5	455	22	AAB86817	Human TNFBP-associ
30	205.5	20.5	455	22	AAB36697	Human tumour necro
31	205.5	20.5	455	22	AAB37677	Human 30 kDa TNF i
32	205.5	20.5	455	23	ABB81649	Human tumour necro
33	205.5	20.5	455	23	AAU75064	Human tumour necro
34	205	20.5	327	14	AAR41688	Murine Fas. Mus m
35	205	20.5	327	16	AAR78611	Murine Fas antigen
36	205	20.5	327	17	AAR92530	mFas sequence. Sy
37	205	20.5	327	20	AAW86241	Fas ligand (FasL)
38	205	20.5	327	21	AAB19344	Amino acid sequenc
39	204.5	20.4	285	18	AAW33359	TBP(20-190)/hCG-al
40	204.5	20.4	455	13	AAR20787	TNF-alpha binding
41	204.5	20.4	658	23	AAM49759	TNF-selectokine pr
42	203	20.3	350	23	ABB81468	Viral CrmB protein
43	202.5	20.2	349	22	AAB50523	Human tumour necro
44	200.5	20.1	139	22	AAB66977	Peptide: SEQ ID 12
45	200.5	20.1	154	21	AAY94711	Tumour necrosis fa

ALIGNMENTS

RESULT 1
AAW80254
ID AAW80254 standard; Protein; 176 AA.
XX
AC AAW80254;
XX
DT 28-JAN-1999 (first entry)
XX
DE Amino acid sequence of protein 7F4.
XX
KW Protein 7F4; differentiation; osteoblast cell; bone growth;
KW bone sarcoma.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..176
FT /note= "mature protein"
XX
PN WO9843998-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1998; 98WO-JP01511.
XX
PR 01-APR-1997; 97JP-0099653.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Kimura N, Toyoshima T;
XX

DR WPI; 1998-568275/48.
DR N-PSDB; AAV68046.
XX
PT Receptor protein inducing differentiation in osteoblast cells - has
PT extracellular region only and can be used for screening substances
PT for treatment of bone growth disorders
XX
PS Claim 1; Pages 29-31; 51pp; Japanese.
XX
CC The present sequence represents a protein designated 7F4. This protein
CC is capable of inducing differentiation in osteoblast cells. The
CC protein may be used to screen compounds for the ability to bind to
CC it, for use as ligands, agonists or antagonists and inhibiting or
CC otherwise altering its differentiation inducing activity. Compounds
CC so identified, as well as the protein itself, DNA encoding it, and
CC antibodies to it, may be used in the treatment of diseases of bone
CC growth and osteoblast differentiation, such as bone sarcomas.
XX
SQ Sequence 176 AA;

Query Match 100.0%; Score 1000; DB 19; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.5e-76;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60

Qy      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120

Qy     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
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RESULT 2
ABG09344
ID ABG09344 standard; Protein; 380 AA.
XX
AC ABG09344;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9335.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS73531.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 39703; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 380 AA;

Query Match 35.0%; Score 350.5; DB 22; Length 380;
Best Local Similarity 57.6%; Pred. No. 1.3e-21;
Matches 72; Conservative 3; Mismatches 17; Indels 33; Gaps 2;

```
Qy       7 VSSLSHWF--------LLLLLLNLFLP------------------------VIFAMPES 33
           ||||| ||        ||||||||  |                        | ||| |
Db      48 VSSLSRWFLWRRLLLLLLLLLLNLPLQKAVHRKATPESAIADCSGPRDCAPWVKFAMLEL 107

Qy      34 YSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELC 93
           :|| || ||| | ||||| | :||||||||:||||||||||||||||| ||| |  | ||
Db     108 HSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILC 167

Qy      94 STCDK 98
           |||||
Db     168 STCDK 172
```

RESULT 3
ABB81467
ID ABB81467 standard; Protein; 204 AA.
XX
AC ABB81467;
XX
DT 29-AUG-2002 (first entry)
XX
DE Murine TACH protein SEQ ID NO:2.
XX
KW TACH; tumour necrosis factor receptor family; TNF receptor; cancer;
KW inflammatory; immunoregulatory; cytostatic; antiinflammatory;
KW gene therapy.
XX
OS Mus sp.
XX
PN WO200228900-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30993.
XX
PR 04-OCT-2000; 2000US-237791P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOX-) APOXIS BIOSCIENCES LTD.
XX
PI Zheng T, Tschopp J, Schneider P;
XX
DR WPI; 2002-507878/54.

DR N-PSDB; ABN89334.
XX
PT Novel isolated tumor necrosis factor receptor family member nucleic
PT acid, termed TACH, useful for diagnosing, treating, preventing or
PT delaying cancer, inflammatory or immunoregulatory condition -
XX
PS Claim 3; Fig 1; 87pp; English.
XX
CC The present invention describes an isolated tumour necrosis factor (TNF)
CC receptor family member, designated TACH (I). (I) has cytostatic and
CC antiinflammatory activities, and can be used in gene therapy. (I) can
CC be used for diagnosing, treating, preventing or delaying cancer,
CC inflammatory or immunoregulatory conditions. (I) is also useful for
CC modulating the activity of cytokines, in screening assays, detection
CC assays (e.g. chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics), and in methods of
CC treatment (e.g. therapeutic and prophylactic). The present sequence
CC represents murine TACH from the present invention.
XX
SQ Sequence 204 AA;

Query Match 28.0%; Score 280; DB 23; Length 204;
Best Local Similarity 37.4%; Pred. No. 5.7e-16;
Matches 55; Conservative 23; Mismatches 67; Indels 2; Gaps 2;

```
Qy      16 LLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKC 75
           ||||| | | |      : :  |  ||::  ::||  | :||::: ||:  | : :|  |
Db       6 LLLLLGLLLRVAVCSVNTITL-CKIGEFKHENLCCLQCSAGTYLRNPCQENHNKSECAPC 64

Qy      76 HPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCT 135
               |    |   :|  || |  ||  || || |:|| |:|: | |       | |  |:
Db      65 DSEHFIDHKNRESECFPCSVCRDDQEEVAKCSRTADRVCQCKQGTYCDSENCLERCHTCS 124

Qy     136 KCPQGIPVLQECNSTANTVCSSSVSNP 162
           || |  |:::||:| :|||    | |
Db     125 SCPDG-RVVRKCNATMDTVCDKFDSEP 150
```

RESULT 4
AAR07450
ID AAR07450 standard; protein; 461 AA.
XX
AC AAR07450;
XX
DT 29-JAN-1991 (first entry)
XX
DE Rat Tumour Necrosis Factor-Receptor from raTNF-R8 cDNA.
XX
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW raTNF-R8.
XX
OS Rat rattus.
XX
PN EP393438-A.
XX
PD 24-OCT-1990.
XX
PF 06-APR-1990; 90EP-0106624.
XX
PR 21-JUN-1989; 89DE-3920282.
PR 21-APR-1989; 89DE-3913101.
XX
PA (BOEH) BOEHRINGER INGELHEIMINT.
XX
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
XX
DR WPI; 1990-321987/43.
DR N-PSDB; AAQ06284.
XX
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
XX
PS Disclosure; Fig 8(1-2); 51pp; German.
XX
CC A rat brain cDNA analogue of the HS913T cDNA library from rat
CC glioma cell line C6 (ATCC CCL107) is prepared in lambda-gt11.
CC The isolated clone raTNF-R8 is used as probe to isolated the entire
CC human TNF receptor, as represented in AAQ06285.
CC See also AAQ06282-Q06285.
XX
SQ Sequence 461 AA;

Query Match 20.9%; Score 209; DB 11; Length 461;
Best Local Similarity 27.4%; Pred. No. 1.2e-09;
Matches 52; Conservative 22; Mismatches 62; Indels 54; Gaps 7;

```
Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |:  |  :: | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN----------WL 166
           ||||:                                  ::|:||::           :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     167 FLLMLIVFCI 176
           | :|   ||
Db     221 GLCLLFFICI 230
```

RESULT 5
AAR85073
ID AAR85073 standard; Protein; 355 AA.
XX
AC AAR85073;
XX
DT 16-APR-1996 (first entry)
XX
DE Cowpox virus T2-equivalent protein.
XX
KW Cowpox virus; immunosuppressive; cytokine antagonist;
KW tumour necrosis factor antagonist; therapeutic; cachexia;
KW septic shock.
XX
OS Cowpox virus.
XX
PN US5464938-A.
XX
PD 07-NOV-1995.
XX
PF 18-AUG-1994; 94US-0292549.
XX
PR 19-OCT-1992; 92US-0963330.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Goodwin RG, Smith CA;
XX
DR WPI; 1995-402861/51.
DR N-PSDB; AAT02472.
XX
PT New soluble viral proteins that bind tumour necrosis factor - for
PT treating cachexia, septic shock, side effects of TNF therapy etc.,
PT also useful in assays, affinity purificn. and antibody prodn.
XX
PS Claim 1; Columns 35-38; 21pp; English.
XX
CC The cowpox virus T2-equivalent protein is a soluble viral protein
CC which binds tumour necrosis factor (TNF), thus inhibiting TNF
CC binding to its receptor. T2 protein is useful (when administered
CC by injection or infusion from sustained release implants, etc.) for
CC treating TNF associated toxicity e.g. side effects of using TNF as

CC an antitumour agent or in cases of cachexia and septic shock where
CC TNF production is excessive.
XX
SQ Sequence 355 AA;

Query Match 20.6%; Score 206.5; DB 16; Length 355;
Best Local Similarity 31.1%; Pred. No. 1.5e-09;
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;

Qy 14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
Db 4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy 71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
Db 64 QCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy 130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
Db 123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179

RESULT 6
AAB50524
ID AAB50524 standard; Protein; 355 AA.
XX
AC AAB50524;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor CRMB protein SEQ ID NO:14.
XX
KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo sapiens.
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US13515.
XX
PR 20-MAY-1999; 99US-0135164.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX
DR WPI; 2001-041051/05.
XX
PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX
PS Disclosure; Fig 2; 285pp; English.
XX
CC The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TRID in the exemplification of the present invention.
XX
SQ Sequence 355 AA;

Query Match 20.6%; Score 206.5; DB 22; Length 355;
Best Local Similarity 31.1%; Pred. No. 1.5e-09;
Matches 55; Conservative 25; Mismatches 72; Indels 25; Gaps 8;

Qy 14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
Db 4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy 71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
Db 64 QCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy 130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
Db 123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179

RESULT 7
AAR07451
ID AAR07451 standard; protein; 455 AA.
XX
AC AAR07451;
XX
DT 29-JAN-1991 (first entry)
XX
DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
XX
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW infectious disease; parasitic disease; cachexia;
KW autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
XX
OS Homo sapiens.
XX
PN EP393438-A.
XX
PD 24-OCT-1990.
XX
PF 06-APR-1990; 90EP-0106624.
XX
PR 21-JUN-1989; 89DE-3920282.
PR 21-APR-1989; 89DE-3913101.
XX
PA (BOEH) BOEHRINGER INGELHEIMINT.
XX
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;
XX
DR WPI; 1990-321987/43.
DR N-PSDB; AAQ06285.
XX
PT DNA encoding TNF binding protein and TNF- receptor - used in
PT tumour treatment and to understand mechanismsm to TNF action
XX
PS Disclosure; Fig 91(1-2); 51pp; German.
XX
CC raTNF-R8 (AAQ06284) was used to screen the HS913T cDNA library.
CC LambdaTNF-R2 encodes the complete human TNF-R2 and was used to
CC construct a plasmid (pADTNF-R) expressing the product the same way
CC as pADTNF-BP (see AAQ06282). The expressed proteins are useful

```
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha). They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also AAQ06282-Q06285.
XX
SQ   Sequence   455 AA;

  Query Match             20.6%;  Score 206.5;  DB 11;  Length 455;
  Best Local Similarity   31.3%;  Pred. No. 2e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :||:    | |:|: | :      ||  :|     |      || |:|   |:| :||  |
Db       3 LSSVPDLLLPLVLVELLVGIYPSAVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 8
AAR24084
ID   AAR24084 standard; Protein; 168 AA.
XX
AC   AAR24084;
XX
DT   05-NOV-1992  (first entry)
XX
DE   Truncated TNF-alpha 55kD receptor.
XX
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   WO9207076-A.
XX
PD   30-APR-1992.
XX
PF   18-OCT-1991;   91WO-GB01826.
XX
PR   18-OCT-1990;   90GB-0022648.
XX
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
XX
PI   Brennan FM,  Feldmann M,  Gray PW,  Turner MJC;
XX
DR   WPI; 1992-167156/20.
DR   N-PSDB; AAQ24445.
XX
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
XX
PS   Example 1; Fig 11; 43pp; English.
XX
CC   This sequence is a truncated TNF-alpha receptor derivative, as
CC   encoded in pdeltaIV. This was produced as described in AAQ24445.
CC   This derivative lacks the membrane proximal 4th subdomain, yet
CC   retains the ability to bind TNF-alpha with high affinity
CC   (10power8 - 10power9 Mpower-1) The deriv. can be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis. The deriv. is given at 10-100ug/dose.
CC   See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX
SQ   Sequence   168 AA;

  Query Match             20.5%;  Score 205.5;  DB 13;  Length 168;
  Best Local Similarity   31.3%;  Pred. No. 8.4e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 9
AAR24080
ID   AAR24080 standard; Protein; 199 AA.
XX
AC   AAR24080;
XX
DT   05-NOV-1992  (first entry)
XX
DE   Truncated TNF-alpha 55kD receptor.
XX
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningits; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   WO9207076-A.
XX
PD   30-APR-1992.
XX
PF   18-OCT-1991;   91WO-GB01826.
XX
PR   18-OCT-1990;   90GB-0022648.
XX
PA   (CHAR-) CHARING CROSS SUNLEY RES CENT.
XX
PI   Brennan FM,  Feldmann M,  Gray PW,  Turner MJC;
XX
DR   WPI; 1992-167156/20.
DR   N-PSDB; AAQ24441.
XX
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
XX
PS   Example; Fig 7; 43pp; English.
XX
CC   This sequence is a truncated TNF-alpha receptor derivative, as encoded
CC   in pTNFRecd. This was produced as described in AAQ24440.
CC   This derivative lacks the 81 carboxyl terminal residues of the
CC   cytoplasmic domain. The derivative could be used in the
CC   regulation of TNF-alpha mediated responses by binding and
CC   sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC   diseases, septic shock, HIV infection, malaria, viral meningitis,
CC   graft versus host disease and autoimmune diseases, esp. rheumatoid
CC   arthritis.
CC   See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX
SQ   Sequence   199 AA;
```

```
  Query Match             20.5%;  Score 205.5;  DB 13;  Length 199;
  Best Local Similarity   31.3%;  Pred. No. 1e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 10
AAW89225
ID   AAW89225 standard; Protein; 211 AA.
XX
AC   AAW89225;
XX
DT   04-MAR-1999  (first entry)
XX
DE   Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.
XX
KW   Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW   OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW   inflammation; apoptosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9849305-A1.
XX
PD   05-NOV-1998.
XX
PF   29-APR-1998;   98WO-US08631.
XX
PR   01-MAY-1997;   97US-0850188.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Wooden S;
XX
DR   WPI; 1999-034661/03.
XX
PT   New chimeric osteoprotegerin polypeptides - contain the
PT   osteoprotegerin dimerisation domain and a heterologous sequence,
PT   useful to treat TNF and TNFR-mediated disorders
XX
PS   Example 1; Fig 4; 92pp; English.
XX
CC   The present invention describes a chimeric polypeptide (A1), comprising
CC   an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC   amino acid sequence. Also described are: (1) a multimer polypeptide
CC   comprising covalently associated A1 monomers; (2) an isolated nucleic
CC   acid encoding A1; (3) an expression vector comprising the nucleic acid
CC   sequence; and (4) a host cell transformed or transfected with the
CC   expression vector so that the nucleic acid is expressible. The products
CC   from the present invention are useful to treat a variety of disorders
CC   including those related to receptor binding. Compositions comprising
CC   tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC   are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC   autoimmune diseases and disorders related to excessive apoptosis. The
CC   chimeras are also useful for detecting molecules which interact with
CC   fused heterologous sequences to identify potential new receptors and
CC   ligands. The present sequence represents a TNFbp/OPG construct from
CC   the example of the present invention for creating TNFbp/OPG fusion
CC   proteins.
XX
SQ   Sequence   211 AA;

  Query Match             20.5%;  Score 205.5;  DB 20;  Length 211;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 11
AAB66979
ID   AAB66979 standard; Protein; 280 AA.
XX
AC   AAB66979;
XX
DT   19-APR-2001  (first entry)
XX
DE   Tnfrl protein.
XX
KW   Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW   multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW   systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW   acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
KW   coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW   endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
KW   ischaemia; Parkinson's disease.
XX
OS   Unidentified.
XX
PN   WO200103719-A2.
XX
PD   18-JAN-2001.
XX
PF   07-JUL-2000; 2000WO-US18667.
XX
PR   09-JUL-1999;   99US-0350670.
PR   09-DEC-1999;   99US-0457647.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Lacey DL,  Calzone FJ,  Chang M,  Senaldi G;
XX
DR   WPI; 2001-103031/11.
XX
PT   Treating conditions leading to bone loss such as rheumatoid arthritis,
PT   multiple sclerosis and asthma, comprises administering an
PT   osteoprotegerin protein in conjunction with e.g. inhibitors of
PT   interleukin and tumor necrosis factor alpha  -
XX
PS   Disclosure; Fig 2; 316pp; English.
XX
CC   The present invention relates to a method for treating conditions leading
CC   to bone loss. The method comprises administering a purified and isolated
CC   osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
CC   in conjunction with other substances such as tumour necrosis factor-alpha
CC   (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC   modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
CC   activating factor (PAF) antagonists. The method is useful for treating
CC   conditions leading to bone loss such as rheumatoid arthritis, multiple
CC   sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC   useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC   graft-versus-host disease (GvHD). Other diseases that can be treated
CC   include acute pancreatitis, Alzheimer's disease, anorexia,
```

CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock. The present sequence was used in a sequence
CC homology comparison.
XX
SQ Sequence 280 AA;

Query Match 20.5%; Score 205.5; DB 22; Length 280;
Best Local Similarity 31.3%; Pred. No. 1.4e-09;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

```
Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |    |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167
```

RESULT 12
AAW89229
ID AAW89229 standard; Protein; 311 AA.
XX
AC AAW89229;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.
XX
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
DR WPI; 1999-034661/03.
XX
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
PS Example 1; Fig 4; 92pp; English.
XX
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents a TNFbp/OPG construct from
CC the example of the present invention for creating TNFbp/OPG fusion
CC proteins.
XX
SQ Sequence 311 AA;

Query Match 20.5%; Score 205.5; DB 20; Length 311;
Best Local Similarity 31.3%; Pred. No. 1.6e-09;
Matches 52; Conservative 22; Mismatches 75; Indels 17; Gaps 6;

```
Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |    |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167
```

RESULT 13
AAW89228
ID AAW89228 standard; Protein; 366 AA.
XX
AC AAW89228;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.
XX
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
DR WPI; 1999-034661/03.
XX
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
PS Example 1; Fig 4; 92pp; English.
XX
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras

```
CC   are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC   autoimmune diseases and disorders related to excessive apoptosis. The
CC   chimeras are also useful for detecting molecules which interact with
CC   fused heterologous sequences to identify potential new receptors and
CC   ligands. The present sequence represents a TNFbp/OPG construct from
CC   the example of the present invention for creating TNFbp/OPG fusion
CC   proteins.
XX
SQ   Sequence   366 AA;

  Query Match             20.5%;  Score 205.5;  DB 20;  Length 366;
  Best Local Similarity   31.3%;  Pred. No. 1.9e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 14
AAR07449
ID   AAR07449 standard; protein; 371 AA.
XX
AC   AAR07449;
XX
DT   29-JAN-1991  (first entry)
XX
DE   Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
XX
KW   Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
KW   pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW   autoimmune disease; shock.
XX
OS   Homo sapiens.
XX
PN   EP393438-A.
XX
PD   24-OCT-1990.
XX
PF   06-APR-1990;   90EP-0106624.
XX
PR   21-JUN-1989;   89DE-3920282.
PR   21-APR-1989;   89DE-3913101.
XX
PA   (BOEH ) BOEHRINGER INGELHEIMINT.
XX
PI   Hauptmann R,  Himmler A,  Maurer-Fogy I,  Stratowa C;
XX
DR   WPI; 1990-321987/43.
DR   N-PSDB; AAQ06282.
XX
PT   DNA encoding TNF binding protein and TNF- receptor - used in
PT   tumour treatment and to understand mechanismsm to TNF action
XX
PS   Disclosure; Fig 1(1-3); 51pp; German.
XX
CC   Clone pTNF-BP15 was used to contruct pADTNF-BP, for transfection of
CC   e.g. COS7 cells.  The expressed proteins are useful
CC   prophylactically and therapeutically to control disorders which
CC   involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
CC   parasitic diseases, shock, cachexia, autoimmune diseases, adult
CC   respiratory distress syndrome etc., or side effects of treatment with
CC   TNG-alpha).  They can also be used as diagnostic reagents for
CC   assaying TNF and in study of TNF-receptor interactions.
CC   See also AAQ06282-Q06285.
XX
SQ   Sequence   371 AA;

  Query Match             20.5%;  Score 205.5;  DB 11;  Length 371;
  Best Local Similarity   31.3%;  Pred. No. 1.9e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 15
AAW89227
ID   AAW89227 standard; Protein; 397 AA.
XX
AC   AAW89227;
XX
DT   04-MAR-1999  (first entry)
XX
DE   Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.
XX
KW   Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW   OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW   inflammation; apoptosis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9849305-A1.
XX
PD   05-NOV-1998.
XX
PF   29-APR-1998;   98WO-US08631.
XX
PR   01-MAY-1997;   97US-0850188.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Wooden S;
XX
DR   WPI; 1999-034661/03.
XX
PT   New chimeric osteoprotegerin polypeptides - contain the
PT   osteoprotegerin dimerisation domain and a heterologous sequence,
PT   useful to treat TNF and TNFR-mediated disorders
XX
PS   Example 1; Fig 4; 92pp; English.
XX
CC   The present invention describes a chimeric polypeptide (A1), comprising
CC   an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC   amino acid sequence. Also described are: (1) a multimer polypeptide
CC   comprising covalently associated A1 monomers; (2) an isolated nucleic
CC   acid encoding A1; (3) an expression vector comprising the nucleic acid
CC   sequence; and (4) a host cell transformed or transfected with the
CC   expression vector so that the nucleic acid is expressible. The products
CC   from the present invention are useful to treat a variety of disorders
CC   including those related to receptor binding. Compositions comprising
CC   tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC   are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC   autoimmune diseases and disorders related to excessive apoptosis. The
CC   chimeras are also useful for detecting molecules which interact with
CC   fused heterologous sequences to identify potential new receptors and
CC   ligands. The present sequence represents a TNFbp/OPG construct from
CC   the example of the present invention for creating TNFbp/OPG fusion
```

```
CC   proteins.
XX
SQ   Sequence   397 AA;

  Query Match             20.5%;  Score 205.5;  DB 20;  Length 397;
  Best Local Similarity   31.3%;  Pred. No. 2.1e-09;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :       ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


Search completed: December 10, 2002, 15:05:52
Job time : 36.7654 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:46 ; Search time 12.4938 Seconds
(without alignments)
414.479 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1000	100.0	176	4	US-09-411-722-1	Sequence 1, Appli
2	858	85.8	148	4	US-09-411-722-2	Sequence 2, Appli
3	206.5	20.6	355	1	US-08-292-549-6	Sequence 6, Appli
4	206.5	20.6	355	4	US-09-006-353A-14	Sequence 14, Appl
5	206.5	20.6	355	4	US-09-573-986-14	Sequence 14, Appl
6	205.5	20.5	167	1	US-08-050-319B-2	Sequence 2, Appli
7	205.5	20.5	167	1	US-08-050-319B-57	Sequence 57, Appl
8	205.5	20.5	167	2	US-08-465-982-2	Sequence 2, Appli
9	205.5	20.5	167	2	US-08-465-982-57	Sequence 57, Appl
10	205.5	20.5	197	4	US-08-828-683A-21	Sequence 21, Appl
11	205.5	20.5	280	3	US-08-974-022-46	Sequence 46, Appl
12	205.5	20.5	280	4	US-08-795-445A-46	Sequence 46, Appl
13	205.5	20.5	280	4	US-08-795-447A-46	Sequence 46, Appl
14	205.5	20.5	280	4	US-08-974-186-46	Sequence 46, Appl
15	205.5	20.5	280	4	US-08-795-446B-46	Sequence 46, Appl
16	205.5	20.5	280	4	US-08-706-945D-132	Sequence 132, App
17	205.5	20.5	455	1	US-08-050-319B-25	Sequence 25, Appl
18	205.5	20.5	455	1	US-08-321-668-2	Sequence 2, Appli
19	205.5	20.5	455	1	US-08-837-941-2	Sequence 2, Appli
20	205.5	20.5	455	2	US-08-126-016-2	Sequence 2, Appli
21	205.5	20.5	455	2	US-08-465-982-25	Sequence 25, Appl
22	205.5	20.5	455	4	US-08-815-469-5	Sequence 5, Appli
23	205.5	20.5	455	4	US-09-006-353A-3	Sequence 3, Appli
24	205.5	20.5	455	4	US-09-527-236A-5	Sequence 5, Appli
25	205.5	20.5	455	4	US-08-054-970-2	Sequence 2, Appli
26	205.5	20.5	455	4	US-09-565-918-4	Sequence 4, Appli
27	205.5	20.5	455	4	US-09-573-986-3	Sequence 3, Appli
28	205	20.5	327	4	US-09-290-640-66	Sequence 66, Appl
29	204.5	20.4	199	1	US-08-050-319B-48	Sequence 48, Appl
30	204.5	20.4	199	2	US-08-465-982-48	Sequence 48, Appl
31	204.5	20.4	285	4	US-08-804-166-6	Sequence 6, Appli
32	204.5	20.4	285	4	US-08-910-991-6	Sequence 6, Appli
33	202.5	20.2	349	4	US-09-006-353A-13	Sequence 13, Appl
34	202.5	20.2	349	4	US-09-573-986-13	Sequence 13, Appl
35	200.5	20.1	139	4	US-08-706-945D-129	Sequence 129, App
36	200.5	20.1	153	2	US-08-219-237B-4	Sequence 4, Appli
37	200.5	20.1	153	4	US-08-477-347-12	Sequence 12, Appl
38	200.5	20.1	153	4	US-08-476-862-3	Sequence 3, Appli
39	200.5	20.1	153	4	US-08-468-560C-4	Sequence 4, Appli
40	200.5	20.1	154	4	US-08-828-683A-12	Sequence 12, Appl
41	200.5	20.1	161	4	US-09-326-394-2	Sequence 2, Appli
42	200.5	20.1	256	4	US-08-804-166-2	Sequence 2, Appli
43	200.5	20.1	256	4	US-08-910-991-2	Sequence 2, Appli
44	200.5	20.1	307	4	US-08-804-166-4	Sequence 4, Appli
45	200.5	20.1	307	4	US-08-910-991-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match 100.0%; Score 1000; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60
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Db       1 MVTFSHVSSLSHWFLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60

Qy      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120

Qy     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
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RESULT 2
US-09-411-722-2
; Sequence 2, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722

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;  CURRENT FILING OATE:  1999-10-01
;  PRIOR APPLICATION NUMBER:  PCT/JP98/01511
;  PRIOR FILING OATE:  1998-04-01
;  PRIOR APPLICATION NUMBER:  JP 9/099653
;  PRIOR FILING OATE:  1997-04-01
;  NUMBER OF SEQ IO NOS:  12
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ IO NO 2
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-411-722-2

  Query Match             85.8%;  Score 858;  OB 4;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-72;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      29 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKONGLH 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ob       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKONGLH 60

Qy      89 OCELCSTCOKOQNMVAOCSATSORKCECQIGLYYYOPKFPESCRPCTKCPQGIPVLQECN 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DCELCSTCOKOQNMVADCSATSORKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120

Qy     149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||
Db     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148


RESULT 3
US-08-292-549-6
; Sequence 6, Application US/08292549
; Patent No. 5464938
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Craig A.
;    APPLICANT:  Goodwin, Raymond G.
;    TITLE OF INVENTION:  Isolated Viral Protein TNF Antagonists
;    NUMBER OF SEQUENCES:  10
;    CORRESPONOENCE ADORESS:
;      AOORESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEOIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-OOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION OATA:
;      APPLICATION NUMBER:  US/08/292,549
;      FILING OATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION OATA:
;      APPLICATION NUMBER:  07/963,330
;      FILING OATE:  10/19/92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia A.
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2602-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ IO NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-292-549-6

  Query Match             20.6%;  Score 206.5;  DB 1;  Length 355;
  Best Local Similarity   31.1%;  Pred. No. 1.1e-11;
  Matches   55;  Conservative   25;  Mismatches   72;  Indels   25;  Gaps    8;

Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Ob       4 YILLLLLSCIIIINSOITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHOCELCS-TCDKOQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           ||  |   ||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Ob      64 QCTPCASOTFTSRNNHLPACLSCNGRCOSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
            |: |   |||          | |  |   |     : | ::|  |    ||  |::
Ob     123 GCKACVSQTKCG1GYGVSGHTPTGOVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 4
US-09-006-353A-14
; Sequence 14, Application US/09006353A
; Patent No. 6261801
;  GENERAL INFORMATION:
;    APPLICANT:  WEI, YING-FEI
;    APPLICANT:  YU, GUO-LIANG
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  RUBEN, STEVEN
;    TITLE OF INVENTION:  TUMOR NECROSIS FACTOR RECEPTOR 5
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADORESS:
;      ADORESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
;      CITY:  ROCKVILLE
;      STATE:  MO
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER REAOABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-OOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION OATA:
;      APPLICATION NUMBER:  US/09/006,353A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROOKES, ANDERS A
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF341
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ IO NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      STRANDEONESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-006-353A-14

  Query Match             20.6%;  Score 206.5;  DB 4;  Length 355;
  Best Local Similarity   31.1%;  Pred. No. 1.1e-11;
  Matches   55;  Conservative   25;  Mismatches   72;  Indels   25;  Gaps    8;

Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNOVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Ob       4 YILLLLLSCIIIINSOITPHEPSNGKCKONEYKRHHLCCLSCPPGTYASRLCOSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHDCELCS-TCOKDQNMVADCSATSORKCECQIGLYYYOPKFPE 129
           ||  |   ||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Ob      64 QCTPCASOTFTSRNNHLPACLSCNGRCOSNQVETRSCNTTHNRICOCAPG-YYCFLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
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```
           |: |   |||          | |  |    |     : | ::|  |    ||  |::
Db    123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 5
US-09-573-986-14
; Sequence 14, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
;  APPLICANT:  Wei, Ying-Fei
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Gentz, Reiner
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION:  Tumor Necrosis Factor Receptor 5
;  FILE REFERENCE:  1488.1280004
;  CURRENT APPLICATION NUMBER: US/09/573,986
;  CURRENT FILING DATE:  2000-05-18
;  NUMBER OF SEQ ID NOS:  27
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-573-986-14

  Query Match             20.6%;  Score 206.5;  DB 4;  Length 355;
  Best Local Similarity   31.1%;  Pred. No. 1.1e-11;
  Matches   55;  Conservative   25;  Mismatches   72;  Indels   25;  Gaps    8;

Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Db       4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           ||  |   ||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Db      64 QCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
           |: |   |||          | |  |    |     : | ::|  |    ||  |::
Db     123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 6
US-08-050-319B-2
; Sequence 2, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319B
;      FILING DATE:  10-May-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-319B-2

  Query Match             20.5%;  Score 205.5;  DB 1;  Length 167;
  Best Local Similarity   31.3%;  Pred. No. 6e-12;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
             :|::  '  | |:|| | :       ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 7
US-08-050-319B-57
; Sequence 57, Application US/08050319B
; Patent No. 5633145
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319B
;      FILING DATE:  10-May-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-319B-57

  Query Match             20.5%;  Score 205.5;  DB 1;  Length 167;
  Best Local Similarity   31.3%;  Pred. No. 6e-12;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
```

```
          :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db      3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy     54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
           ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 8
US-08-465-982-2
; Sequence 2, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-982-2

  Query Match             20.5%;  Score 205.5;  DB 2;  Length 167;
  Best Local Similarity   31.3%;  Pred. No. 6e-12;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy      7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
          :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db      3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy     54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
           ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 9
US-08-465-982-57
; Sequence 57, Application US/08465982
; Patent No. 5863786
;  GENERAL INFORMATION:
;    APPLICANT:  M.Feldmann, P.W. Gray,
;    APPLICANT:  M.J.C. Turner, F.M Brennan
;    TITLE OF INVENTION:  Modified human TNFalpha (Tumor
;    TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reed & Robbins
;      STREET:  635 Bryant Street
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,982
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,319
;      FILING DATE:  10-May-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Robbins, Roberta L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  5150-0030
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  167 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-982-57

  Query Match             20.5%;  Score 205.5;  DB 2;  Length 167;
  Best Local Similarity   31.3%;  Pred. No. 6e-12;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy      7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
          :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db      3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy     54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
           ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 10
US-08-828-683A-21
; Sequence 21, Application US/08828683A
; Patent No. 6469144
;  GENERAL INFORMATION:
;       APPLICANT: Ashkenazi, Avi J.
;       TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
```

```
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;          COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;          CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/828,683A
;            FILING DATE: 31-Mar-1997
;            CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/625328
;            FILING DATE: 1-Apr-1996
;            APPLICATION NUMBER: 08/710802
;            FILING DATE: 23-Sep-1996
;          ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P1007P1
;          TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;     INFORMATION FOR SEQ ID NO: 21:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 197 amino acids
;            TYPE: AMINO ACID
;            TOPOLOGY: Linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-828-683A-21

  Query Match             20.5%;  Score 205.5;  DB 4;  Length 197;
  Best Local Similarity   31.3%;  Pred. No. 7.2e-12;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |    |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 11
US-08-974-022-46
; Sequence 46, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-46

  Query Match             20.5%;  Score 205.5;  DB 3;  Length 280;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           | |:   | :|  :    |  |: |  |  |    |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 12
US-08-795-445A-46
; Sequence 46, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
```

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-445A-46

  Query Match             20.5%;  Score 205.5;  DB 4;  Length 280;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
            ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 13
US-08-795-447A-46
; Sequence 46, Application US/08795447A
; Patent No. 6284728
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-447A-46

  Query Match             20.5%;  Score 205.5;  DB 4;  Length 280;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
            ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 14
US-08-974-186-46
; Sequence 46, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-186-46

  Query Match             20.5%;  Score 205.5;  DB 4;  Length 280;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
            ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 15
US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
```

```
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-446B-46

  Query Match             20.5%;  Score 205.5;  DB 4;  Length 280;
  Best Local Similarity   31.3%;  Pred. No. 1.1e-11;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |      | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


Search completed: December 10, 2002, 15:08:20
Job time : 13.4938 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:04:21 ; Search time 15.7531 Seconds
(without alignments)
1074.054 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215.5	21.6	454	1	GQMST1	tumor necrosis fac
2	210	21.0	461	1	GQRTT1	tumor necrosis fac
3	205.5	20.5	455	1	GQHUT1	tumor necrosis fac
4	205	20.5	327	2	A46484	apoptosis-mediatin
5	204	20.4	348	2	T28623	hypothetical prote
6	202.5	20.2	349	2	D72175	G2R protein - vari
7	202.5	20.2	349	2	D36858	gene G4R protein -
8	194	19.4	324	2	JC2395	Fas antigen precur
9	193.5	19.4	461	2	JC4302	tumor necrosis fac
10	189.5	18.9	335	2	A40036	apoptosis-mediatin
11	184	18.4	651	2	JC7705	death receptor-6 -
12	183	18.3	427	1	GQHUN	nerve growth facto
13	177	17.7	314	2	I37383	FAS soluble protei
14	171	17.1	425	1	A26431	nerve growth facto
15	167.5	16.8	326	1	GQVZML	T2 protein - myxom
16	166.5	16.7	416	1	JN0006	nerve growth facto
17	164	16.4	325	2	B43692	T2 protein - rabbi
18	152	15.2	461	1	A35356	tumor necrosis fac
19	150	15.0	271	2	S12783	OX40 antigen precu
20	150	15.0	435	2	I54182	tumor necrosis fac
21	149	14.9	595	2	A42086	CD30 antigen precu
22	148	14.8	250	1	A49053	CD27 antigen precu
23	145	14.5	260	1	A46517	CD27 antigen precu
24	145	14.5	474	2	B38634	tumor necrosis fac
25	144	14.4	277	2	I37552	OX40 homolog - hum
26	142.5	14.2	459	2	I48854	gene murine tumour
27	140.5	14.1	493	2	JC5486	membrane glycoprot
28	138	13.8	305	2	A46476	B cell-associated
29	136.5	13.7	1790	1	MMFFB1	laminin beta-1 cha
30	130	13.0	256	2	B32393	T-cell antigen 4-1
31	129	12.9	1827	2	T34288	hypothetical prote
32	128.5	12.8	272	2	I48700	gene ox40 protein
33	126.5	12.7	1193	2	A44018	laminin B2t chain
34	125.5	12.6	1192	2	S69000	laminin gamma 2 ch
35	123.5	12.3	255	2	I38426	lymphocyte activat
36	122	12.2	435	2	S40993	hypothetical prote
37	121.5	12.2	1274	2	T42017	cysteine rich prot
38	120	12.0	1609	1	MMHUB2	laminin gamma-1 ch
39	120	12.0	4391	2	A38096	perlecan precursor
40	118	11.8	570	2	T37314	probable kexin (EC
41	118	11.8	942	2	D87803	protein bli-4D [im
42	117	11.7	1548	2	S34583	serine proteinase
43	116	11.6	557	2	A48434	variant-specific s
44	115.5	11.6	1372	2	T25933	hypothetical prote
45	115.5	11.6	1808	2	T15099	hypothetical prote

ALIGNMENTS

RESULT 1
GQMST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R;Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A;Reference number: I54532; MUID:94245292; PMID:8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis fact
A;Reference number: I57826; MUID:93156721; PMID:8381516

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A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             21.6%;  Score 215.5;  DB 1;  Length 454;
  Best Local Similarity   28.1%;  Pred. No. 2.4e-09;
  Matches   52;  Conservative   23;  Mismatches   61;  Indels   49;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :|| |  ||:: : |  |     | :|  |||| | | |  |
Db      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 103

Qy      95 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
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Db     104 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN-----WLFLLML 171
           | ||||:                                ::|:||::      | |::|
Db     161 TQNTVCNCHAGFFLRESECVPCSHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVIL 220

Qy     172 IVFCI 176
           :  |:
Db     221 LGLCL 225


RESULT 2
GQRTT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             21.0%;  Score 210;  DB 1;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 6.4e-09;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |  :  || |  ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQNHVRQCLSCK 103

Qy      95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |:  |  :: | |  |  | |    |  |  :  |  |  |: |  |  |  |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN-----------WL 166
           ||||:                                ::|:||::           :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     167 FLLMLIVFCI 176
           | :|   ||
Db     221 GLCLLFFICI 230


RESULT 3
GQHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231;
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to
A;Reference number: A38208; MUID:92250049; PMID:1315717
A;Accession: A38208
A;Molecule type: DNA
A;Residues: 1-455 <FUC>
A;Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A;Reference number: A34899; MUID:90235284; PMID:2158862
A;Accession: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <LOE>
A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A;Experimental source: placenta
A;Note: part of this sequence, including the amino end of the mature protein, confirm
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A;Reference number: A34900; MUID:90235285; PMID:2158863
A;Accession: A34900
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: A36555
A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',16
A;Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A;Reference number: A38281; MUID:91017509; PMID:2170974
A;Accession: A38281
A;Molecule type: mRNA
```

A;Residues: 1-455 <GRA>
A;Cross-references: GB:M37764
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
le form of the receptor.
A;Reference number: S12057; MUID:91006021; PMID:1698610
A;Accession: S12057
A;Molecule type: mRNA
A;Residues: 1-455 <NOP>
A;Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R;Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
A;Molecule type: DNA
A;Residues: 1-13 <KEM>
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci lII, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factc
tients.
A;Reference number: A38258; MUID:91062364; PMID:2174164
A;Accession: A38258
A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
A;Reference number: A60594; MUID:89171156; PMID:2924890
A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
  Query Match             20.5%;  Score 205.5;  DB 1;  Length 455;
  Best Local Similarity   31.3%;  Pred. No. 1.4e-08;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
           :|::    | |:|| | :      ||  :|     |      || |:|   |:| :||  |
Db       3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167
```

RESULT 4
A46484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki
J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas
A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Accession: A46484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <WAT>
A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A;Experimental source: BAM3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable elem
A;Reference number: A47254; MUID:93189576; PMID:7680478
A;Accession: A47254
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
A;Cross-references: GB:S56490; NID:g29B505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>

```
  Query Match             20.5%;  Score 205;  DB 2;  Length 327;
  Best Local Similarity   31.5%;  Pred. No. 1.2e-08;
  Matches   45;  Conservative   23;  Mismatches   67;  Indels    8;  Gaps    5;

Qy      37 NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCST 95
           || :| ||    ||: |  |      ||:      |  |  |  :  |::    |  |:
Db      43 NCSEGLYQGGPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTL 102

Qy      96 CDKDQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANT 153
           ||::  :  :  |: | : ||:|:   :| |    | |  |  |  |   |: | :|:||
Db     103 CDEEHGLEVETNCTLTQNTKCKCKPD-FYCDSPGCEHCVRCASCEHG--TLEPCTATSNT 159

Qy     154 VCSSSVSNPRNWLFLLMLIVFCI 176
             |     :||| |:|| ::|  |
Db     160 NCRK--QSPRNRLWLLTILVLLI 180
```

RESULT 5
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 20.4%; Score 204; DB 2; Length 348;
Best Local Similarity 34.0%; Pred. No. 1.5e-08;
Matches 51; Conservative 20; Mismatches 67; Indels 12; Gaps 6;

```
Qy     16 LLLLLNLFLPVIFAMPESYSF-----NCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQG 70
          :| |  |||  |    ::  :      | | ||: :::|| :|| ||:    |    |
Db      4 VLYLYILFLSCIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNT 62

Qy     71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
          ||  |  |||| ::| |  |  |: |: :|     |: | :| |||  | ||   |
Db     63 QCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPG-YYCLLKGSS 121

Qy    130 SCRPC---TKCPQGIPVLQECNSTANTVCS 156
           |: |   |||  |  |     |  : :||
Db    122 GCKACVSQTKCGIGYGVSGH-TSVGDVICS 150
```

RESULT 6
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 20.2%; Score 202.5; DB 2; Length 349;
Best Local Similarity 33.8%; Pred. No. 1.9e-08;
Matches 52; Conservative 18; Mismatches 65; Indels 19; Gaps 7;

```
Qy     16 LLLLLNLFLPVI---------FAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIP 66
          :| |  |||  |         :  |      | | ||: :::|| :|| ||:    |
Db      4 VLYLYILFLSCIINGRDAAPYTPPNG---KCKDTEYKRHNLCCLSCPPGTYASRLCD-S 59

Qy     67 HTQGQCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDP 125
          |  ||  |  |||| ::| |  |  |:  |: :|     |: | :| |||  | ||
Db     60 KTNTQCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPG-YYCLL 118

Qy    126 KFPESCRPC---TKCPQGIPVLQECNSTANTVCS 156
          |    |: |   |||  |  |     |  : :||
Db    119 KGSSGCKACVSQTKCGIGYGVSGH-TSVGDVICS 151
```

RESULT 7
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protect
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 20.2%; Score 202.5; DB 2; Length 349;
Best Local Similarity 33.8%; Pred. No. 1.9e-08;
Matches 52; Conservative 18; Mismatches 65; Indels 19; Gaps 7;

```
Qy     16 LLLLLNLFLPVI---------FAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIP 66
          :| |  |||  |         :  |      | | ||: :::|| :|| ||:    |
Db      4 VLYLYILFLSCIINGRDAAPYTPPNG---KCKDTEYKRHNLCCLSCPPGTYASRLCD-S 59

Qy     67 HTQGQCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDP 125
          |  ||  |  |||| ::| |  |  |:  |: :|     |: | :| |||  | ||
Db     60 KTNTQCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPG-YYCLL 118

Qy    126 KFPESCRPC---TKCPQGIPVLQECNSTANTVCS 156
          |    |: |   |||  |  |     |  : :||
Db    119 KGSSGCKACVSQTKCGIGYGVSGH-TSVGDVICS 151
```

RESULT 8
JC2395
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat 1
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468

```
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62,'RFT' <KI2>
A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <MAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>

  Query Match             19.4%;  Score 194;  DB 2;  Length 324;
  Best Local Similarity   27.1%;  Pred. No. 8.2e-08;
  Matches   52;  Conservative   26;  Mismatches   74;  Indels   40;  Gaps    9;

Qy      17 LLLLNLFLPVIFAMPE--------------------SYSFNCPDGEYQSNDVCCKTCP 54
           :| :   ||:: | ||                    || :| ||    ||: |
Db       1 MLWIMAVLPLVLAGPELNVRMQGTDSIFEGLELKRSVRETDNNCSEGLYQVGPFCCQPCQ 60

Qy      55 SGTFVKAPCKIPHTQGQCEKCHPGT----FTGKDNGLHDCELCSTCDKDQNMVAD--CSA 108
            |      |    | |    ||| |    :| : :    |  |: ||:   :  :  |:
Db      61 PGERKVKDCT---TSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTR 117

Qy     109 TSDRKCECQIGLYYYDPKFPESCRPCTKCPQGI-PVLQECNSTANTVCSSSVSNPR-NWL 166
           | : || |:   :| :    : |  || |  |:  :|: |  |:|| |    || :  ||
Db     118 TQNTKCRCKEN-FYCNASLCDHCYHCTSC--GLEDILEPCTRTSNTKCKKQSSNYKLLWL 174

Qy     167 FLL----MLIVF 174
             :|    :| ||
Db     175 LILPGLAILFVF 186


RESULT 9
JC4302
tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645; PMID:7590278
A;Accession: JC4302
A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A;Accession: PC4093
A;Molecule type: protein
A;Residues: 1-7 <SU2>
A;Experimental source: kidney cell line 15
C;Genetics:
A;Gene: tnfr
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;211-231/Domain: transmembrane #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.4%;  Score 193.5;  DB 2;  Length 461;
  Best Local Similarity   32.3%;  Pred. No. 1.1e-07;
  Matches   41;  Conservative   17;  Mismatches   58;  Indels   11;  Gaps    5;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   |:  :|| |  ||::   |  |     | :|  |||| :| |  |  ||
Db      44 CPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTASENHLTQCLSCS 103

Qy      95 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           |  : : |  : |:   |  | |   |   |: :  |   |  |: || |  |   |
Db     104 KCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLF--QCLNCSLCPNG-TVQLPCLE 160

Qy     150 TANTVCS 156
             :|:|:
Db     161 KQDTICN 167


RESULT 10
A40036
apoptosis-mediating surface antigen Fas precursor - human
N;Alternate names: surface antigen APO-1
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C;Accession: A40036; S24543; A38142
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Ha
Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m
A;Reference number: A40036; MUID:91309137; PMID:1713127
A;Accession: A40036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A;Reference number: S24543
A;Accession: S24543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <KRA>
A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; R
J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a memb
A;Reference number: A38142; MUID:92268122; PMID:1375228
A;Accession: A38142
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-134,'Q',136-335 <OEH>
A;Experimental source: SKW6.4 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse
C;Genetics:
A;Gene: GDB:APT1
A;Cross-references: GDB:132671; OMIM:134637
A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
C;Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4>
F;174-190/Domain: transmembrane #status predicted <TMM>

  Query Match             18.9%;  Score 189.5;  DB 2;  Length 335;
  Best Local Similarity   30.9%;  Pred. No. 1.8e-07;
  Matches   42;  Conservative   19;  Mismatches   68;  Indels    7;  Gaps    5;

Qy      40 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 98
           :| :     | | || |      | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109

Qy      99 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             :  :  |: | : || |:   :: :    | | |||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     157 SSVSNPR-NWLFLLML 171
             |     || ||:|
Db     167 EEGSRSNLGWLCLLLL 182
```

```
RESULT 11
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match             18.4%;  Score 184;  DB 2;  Length 651;
  Best Local Similarity   30.0%;  Pred. No. 7.5e-07;
  Matches   45;  Conservative   24;  Mismatches   65;  Indels   16;  Gaps    5;

Qy      17 LLLLNLFLPVIFAMP----ESYSFNCPDGEY------QSNDVCCKTCPSGTFVKAPCKIP 66
           :| | :||    | |    |  : : | |:|       : :: |  ||:||:|   |
Db       9 VLPLLVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC-TK 67

Qy      67 HTQGQCEKCHPGTFTGKDNGLHDCELC-STCDKDQNMVADCSATSDRKCECQIGLYYYDP 125
            |  :|  |  |||| :||:  |  |   |:        |:| :||:| |  | :
Db      68 STLRECSPCPDGTFTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF---- 123

Qy     126 KFPESCRPCTKCPQGIPVLQECNSTANTVC 155
           :  ::| | | || |  | ::   | :  |
Db     124 QINDTCVPYTVCPVGWGVRKKGTETEDVRC 153


RESULT 12
GQHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factc
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleoti
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor recept
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C;Comment: The cysteine-rich region of the extracellular domain may form part or all
C;Comment: This protein is thought to form a high-affinity receptor when it associate
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             18.3%;  Score 183;  DB 1;  Length 427;
  Best Local Similarity   33.8%;  Pred. No. 6.7e-07;
  Matches   48;  Conservative   11;  Mismatches   71;  Indels   12;  Gaps    5;

Qy      15 LLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEK 74
           |||||| : |       |:    || | |  :  ||| |  |  |  ||     |  ||
Db      16 LLLLLLGVSLG---GAKEA----CPTGLYTHSGECCKACNLGEGVAQPCGA--NQTVCEP 66

Qy      75 CHPG-TFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRP 133
           |    ||:   :    |: |: |   |:| | |    |  | | |  ||  :    |
Db      67 CLDSVTFSDVVSATEPCKPCTECVGLQSMSAPCVEADDAVCRCAYG--YYQDETTGRCEA 124

Qy     134 CTKCPQGIPVLQECNSTANTVC 155
           |  |  |  ::  |    ||||
Db     125 CRVCEAGSGLVFSCQDKQNTVC 146


RESULT 13
I37383
FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I37383
R;Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule
A;Reference number: I37383; MUID:95181785; PMID:7533181
A;Accession: I37383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539

  Query Match             17.7%;  Score 177;  DB 2;  Length 314;
  Best Local Similarity   30.1%;  Pred. No. 1.6e-06;
  Matches   37;  Conservative   18;  Mismatches   62;  Indels    6;  Gaps    4;

Qy      40 DGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPG-TFTGKDNGLHDCELCSTCDK 98
           :| :     | | || |     | :   :  |  |  |  :| | :    |  |  ||:
Db      50 EGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109
```

```
Qy      99 DQNMVAD--CSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
           :  :  |: | : || |:   :: :    | | |||||  ||  ::||  |:|| |
Db     110 GHGLEVEINCTRTQNTKCRCKPN-FFCNSTVCEHCDPCTKCEHGI--IKECTLTSNTKCK 166

Qy     157 SSV 159
           |
Db     167 EEV 169


RESULT 14
A26431
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             17.1%;  Score 171;  DB 1;  Length 425;
  Best Local Similarity   32.6%;  Pred. No. 5.4e-06;
  Matches   46;  Conservative   11;  Mismatches   76;  Indels    8;  Gaps    4;

Qy      16 LLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKC 75
           | ||| | | |     :     |  | |  :  ||| |  |  |  ||     |  || |
Db      14 LRLLLLLILGVSSGGAKE---TCSTGLYTHSGECCKACNLGEGVAQPCGA--NQTVCEPC 68

Qy      76 HPG-TFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPC 134
               ||:   :    |: |: |   |:| | |    |  | | |  |  ||  :    |  |
Db      69 LDNVTFSDVVSATEPCKPCTECLGLQSMSAPCVEADDAVCRCAYG--YYQDEETGHCEAC 126

Qy     135 TKCPQGIPVLQECNSTANTVC 155
           : |  |  ::  |    ||||
Db     127 SVCEVGSGLVFSCQDKQNTVC 147


RESULT 15
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosi
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             16.8%;  Score 167.5;  DB 1;  Length 326;
  Best Local Similarity   30.0%;  Pred. No. 8.4e-06;
  Matches   45;  Conservative   18;  Mismatches   76;  Indels   11;  Gaps    7;

Qy      14 FLLLLLLNLFLPVIFAMPESYSFN---CPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQG 70
           | | |||   ::  ::     |  :   |   :|: : :|| :|| |::    |  | :
Db       2 FRLTLLL-AYVACVYGGGAPYGADRGKCRGNDYEKDGLCCTSCPPGSYASRLCG-PGSDT 59

Qy      71 QCEKCHPGTFTGKDNGLHDCELC-STCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           |  |   |||   |    |  |   |    :    |  | || |:|  | |    |  |
Db      60 VCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCDKTRDRVCDCSAGNYCL-LKGQE 118

Qy     130 SCRPC---TKCPQGIPVLQECNSTANTVCS 156
           || |   |||| |  |      | : :|:
Db     119 GCRICAPKTKCPAGYGVSGH-TRTGDVLCT 147


Search completed: December 10, 2002, 15:07:51
Job time : 17.7531 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 10, 2002, 15:05:57 ; Search time 8.14815 Seconds
(without alignments)
350.834 Million cell updates/sec

Title: US-09-855-266A-1
Perfect score: 1000
Sequence: 1 MVTFSHVSSLSHWFLLLLLL.....SSVSNPRNWLFLLMLIVFCI 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1000	100.0	176	10	US-09-855-266A-1	Sequence 1, Appli
2	858	85.8	148	10	US-09-855-266A-2	Sequence 2, Appli
3	213.5	21.3	162	10	US-09-798-789-13	Sequence 13, Appl
4	212.5	21.2	123	10	US-09-855-266A-13	Sequence 13, Appl
5	209	20.9	461	9	US-09-898-234-15	Sequence 15, Appl
6	209	20.9	461	9	US-09-899-429A-25	Sequence 25, Appl
7	209	20.9	461	10	US-09-899-422-15	Sequence 15, Appl
8	207.5	20.8	162	10	US-09-798-789-15	Sequence 15, Appl
9	206.5	20.6	355	10	US-09-826-212-14	Sequence 14, Appl
10	206.5	20.6	355	10	US-09-935-727-16	Sequence 16, Appl
11	205.5	20.5	201	9	US-09-899-429A-14	Sequence 14, Appl
12	205.5	20.5	211	9	US-09-899-429A-8	Sequence 8, Appli
13	205.5	20.5	371	9	US-09-898-234-12	Sequence 12, Appl
14	205.5	20.5	371	10	US-09-899-422-12	Sequence 12, Appl
15	205.5	20.5	455	9	US-09-898-234-2	Sequence 2, Appli
16	205.5	20.5	455	9	US-09-898-234-17	Sequence 17, Appl
17	205.5	20.5	455	9	US-09-756-854-5	Sequence 5, Appli
18	205.5	20.5	455	9	US-09-899-429A-2	Sequence 2, Appli
19	205.5	20.5	455	9	US-09-899-429A-27	Sequence 27, Appl
20	205.5	20.5	455	9	US-10-041-574-5	Sequence 5, Appli
21	205.5	20.5	455	10	US-09-826-212-3	Sequence 3, Appli
22	205.5	20.5	455	10	US-09-333-966-5	Sequence 5, Appli
23	205.5	20.5	455	10	US-09-027-287-3	Sequence 3, Appli
24	205.5	20.5	455	10	US-09-874-138-3	Sequence 3, Appli
25	205.5	20.5	455	10	US-09-840-707A-16	Sequence 16, Appl
26	205.5	20.5	455	10	US-09-252-656B-3	Sequence 3, Appli
27	205.5	20.5	455	10	US-09-899-422-2	Sequence 2, Appli
28	205.5	20.5	455	10	US-09-899-422-17	Sequence 17, Appl
29	205.5	20.5	455	10	US-09-935-727-5	Sequence 5, Appli
30	205.5	20.5	455	12	US-10-005-842-3	Sequence 3, Appli
31	205.5	20.5	455	12	US-10-120-397-2	Sequence 2, Appli
32	205	20.5	204	10	US-09-948-018-18	Sequence 18, Appl
33	205	20.5	327	10	US-09-802-669-66	Sequence 66, Appl
34	204.5	20.4	162	10	US-09-798-789-20	Sequence 20, Appl
35	204.5	20.4	285	10	US-09-756-186-6	Sequence 6, Appli
36	203.5	20.3	162	10	US-09-798-789-19	Sequence 19, Appl
37	202.5	20.2	162	10	US-09-798-789-11	Sequence 11, Appl
38	202.5	20.2	349	10	US-09-826-212-13	Sequence 13, Appl
39	202.5	20.2	349	10	US-09-935-727-15	Sequence 15, Appl
40	202	20.2	190	9	US-09-899-429A-18	Sequence 18, Appl
41	202	20.2	200	9	US-09-899-429A-12	Sequence 12, Appl
42	201.5	20.2	162	10	US-09-798-789-14	Sequence 14, Appl
43	201	20.1	371	9	US-09-899-429A-22	Sequence 22, Appl
44	200.5	20.1	153	10	US-09-800-909-3	Sequence 3, Appli
45	200.5	20.1	153	10	US-09-884-987-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match 100.0%; Score 1000; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MVTFSHVSSLSHWFLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MVTFSHVSSLSHWFLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVK 60

Qy      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 APCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCECQIGL 120

Qy     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 YYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLMLIVFCI 176
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RESULT 2
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
;  APPLICANT: Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE: 06501-040002
;  CURRENT APPLICATION NUMBER: US/09/855,266A
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/411,722
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: PCT/JP98/01511
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: JP 9/099653
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-855-266A-2

  Query Match             85.8%;  Score 858;  DB 10;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-62;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      29 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60

Qy      89 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120

Qy     149 STANTVCSSSVSNPRNWLFLLMLIVFCI 176
           ||||||||||||||||||||||||||||
Db     121 STANTVCSSSVSNPRNWLFLLMLIVFCI 148


RESULT 3
US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-13

  Query Match             21.3%;  Score 213.5;  DB 10;  Length 162;
  Best Local Similarity   35.2%;  Pred. No. 7.8e-11;
  Matches   44;  Conservative   15;  Mismatches   59;  Indels    7;  Gaps    4;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| | ||  ||
Db       5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRDCLQCS 64

Qy      95 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 151
           | |    |  : |:   |  | |:   | :|| :    |  |: | |  |   |
Db      65 QCKKHDGQVEISSCTVDRDTVCGCRKNQYRHYDHENRFYCFNCSLCLNG-TVHLSCQEKQ 123

Qy     152 NTVCS 156
           ||||:
Db     124 NTVCT 128


RESULT 4
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
;  APPLICANT: Kimura, Naoki
;  APPLICANT:  Toyoshima, Tomoko
;  TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;  FILE REFERENCE: 06501-040002
;  CURRENT APPLICATION NUMBER: US/09/855,266A
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/411,722
;  PRIOR FILING DATE: 1999-10-01
;  PRIOR APPLICATION NUMBER: PCT/JP98/01511
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: JP 9/099653
;  PRIOR FILING DATE: 1997-04-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-855-266A-13

  Query Match             21.2%;  Score 212.5;  DB 10;  Length 123;
  Best Local Similarity   35.7%;  Pred. No. 7.3e-11;
  Matches   45;  Conservative   13;  Mismatches   57;  Indels   11;  Gaps    5;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |     | :|  ||||   | | |  |
Db       1 CPGGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 60

Qy      95 TCDKDQNMV--ADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |: : |  : | |  |  | |   |   |  :  |   |  |: |  |  |   |
Db      61 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 117

Qy     150 TANTVC 155
           | ||||
Db     118 TQNTVC 123


RESULT 5
US-09-898-234-15
; Sequence 15, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
```

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;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-898-234-15

  Query Match            20.9%;  Score 209;  DB 9;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 4.7e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |:  |  :: | |  |  | |    |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN----------WL 166
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     167 FLLMLIVFCI 176
             | :|   ||
Db     221 GLCLLFFICI 230


RESULT 6
US-09-899-429A-25
; Sequence 25, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-899-429A-25

  Query Match            20.9%;  Score 209;  DB 9;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 4.7e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |:  |  :: | |  |  | |    |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN----------WL 166
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     167 FLLMLIVFCI 176
             | :|   ||
Db     221 GLCLLFFICI 230


RESULT 7
US-09-899-422-15
; Sequence 15, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: raTNF-R8
US-09-899-422-15

  Query Match            20.9%;  Score 209;  DB 10;  Length 461;
  Best Local Similarity   27.4%;  Pred. No. 4.7e-10;
  Matches   52;  Conservative   22;  Mismatches   62;  Indels   54;  Gaps    7;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   ::| :||  |  ||:: : |  |  :  ||  | ||||   | :  |  |
Db      44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCELSHKGTFTASQNHVRQCLSCK 103

Qy      95 TCDKD--QNMVADCSATSDRKCEC---QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNS 149
           || |:  |  :: | |  |  | |    |   |  :  |   |  |: |  |  |   |
Db     104 TCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHF--QCVDCSPCFNG-TVTIPCKE 160

Qy     150 TANTVCS--------------------------------SSVSNPRN----------WL 166
             ||||:                                ::|:||::          :|
Db     161 KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFL 220

Qy     167 FLLMLIVFCI 176
             | :|   ||
Db     221 GLCLLFFICI 230
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RESULT 8
US-09-798-789-15
; Sequence 15, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
;  APPLICANT: Dahiyat, Bassil
;  APPLICANT:  Filikov, Anton
;  TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
;  TITLE OF INVENTION:  VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: A-68990-1/RFT/RMS/RMK
;  CURRENT APPLICATION NUMBER: US/09/798,789
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: US 60/186,427
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  synthetic
US-09-798-789-15

  Query Match             20.8%;  Score 207.5;  DB 10;  Length 162;
  Best Local Similarity   34.4%;  Pred. No. 2.4e-10;
  Matches   43;  Conservative   17;  Mismatches   58;  Indels    7;  Gaps    4;

Qy      38 CPDGEY---QSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCS 94
           || |:|   |:| :||  |  ||::   |  |     | :|  |:||  :| |  | |||
Db       5 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENWLRRCLLCS 64

Qy      95 TCDKDQNMV--ADCSATSDRKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTA 151
            | |::  |  : |:   |  | |:   | :|  :    |  |: |  |  |   |
Db      65 KCRKEEGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQ 123

Qy     152 NTVCS 156
           ||||:
Db     124 NTVCT 128


RESULT 9
US-09-826-212-14
; Sequence 14, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
;  APPLICANT: Wei, Ying-Fei
;  APPLICANT:  Gentz, Reiner
;  APPLICANT:  Ruben, Steven
;  APPLICANT:  Ni, Jian
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
;  FILE REFERENCE: 1488.1280006
;  CURRENT APPLICATION NUMBER: US/09/826,212
;  CURRENT FILING DATE:  2001-04-05
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-212-14

  Query Match             20.6%;  Score 206.5;  DB 10;  Length 355;
  Best Local Similarity   31.1%;  Pred. No. 5.9e-10;
  Matches   55;  Conservative   25;  Mismatches   72;  Indels   25;  Gaps    8;

Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Db       4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           || |  ||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Db      64 QCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
           |: |   |||          | |  |   |     : | ::|  |    ||  |::
Db     123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 10
US-09-935-727-16
; Sequence 16, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-727-16

  Query Match             20.6%;  Score 206.5;  DB 10;  Length 355;
  Best Local Similarity   31.1%;  Pred. No. 5.9e-10;
  Matches   55;  Conservative   25;  Mismatches   72;  Indels   25;  Gaps    8;

Qy      14 FLLLLLLNLFLPV--IFAMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPC-KIPHTQG 70
           ::||||||:  : :       |  :  | | ||: : :|| :|| ||:    |    :|
Db       4 YILLLLLSCIIIINSDITPHEPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTNT 63

Qy      71 QCEKCHPGTFTGKDNGLHDCELCS-TCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPE 129
           || |  ||| ::| |  |  |:  || :|     |: | :| |:|  | ||   |
Db      64 QCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGSS 122

Qy     130 SCRPC---TKC----------PQGIPVLQEC-----NSTANTV--CSSSVSNPRNWL 166
           |: |   |||          | |  |   |     : | ::|  |    ||  |::
Db     123 GCKACVSQTKCGIGYGVSGHTPTGDVVCSPCGLGTYSHTVSSVDKCEPVPSNTFNYI 179


RESULT 11
US-09-899-429A-14
; Sequence 14, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
```

```
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: recombinant
;   OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-14

  Query Match             20.5%;  Score 205.5;  DB 9;  Length 201;
  Best Local Similarity   31.3%;  Pred. No. 4.2e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
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Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
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Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
             | |:   | :|  :    |  |: |  |  |   |    ||||:
Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 12
US-09-899-429A-8
; Sequence 8, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: recombinant
;   OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-8

  Query Match             20.5%;  Score 205.5;  DB 9;  Length 211;
  Best Local Similarity   31.3%;  Pred. No. 4.4e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
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Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
             ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db      63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy     112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
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Db     123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 13
US-09-898-234-12
; Sequence 12, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 371
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
;   OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-898-234-12

  Query Match             20.5%;  Score 205.5;  DB 9;  Length 371;
  Best Local Similarity   31.3%;  Pred. No. 7.4e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy       7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
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Qy      54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
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Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
          | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 14
US-09-899-422-12
; Sequence 12, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 371
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
;   OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-899-422-12

  Query Match             20.5%;  Score 205.5;  DB 10;  Length 371;
  Best Local Similarity   31.3%;  Pred. No. 7.4e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy      7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
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Db      3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy     54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
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Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
          | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


RESULT 15
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-898-234-2

  Query Match             20.5%;  Score 205.5;  DB 9;  Length 455;
  Best Local Similarity   31.3%;  Pred. No. 8.9e-10;
  Matches   52;  Conservative   22;  Mismatches   75;  Indels   17;  Gaps    6;

Qy      7 VSSLSHWFLLLLLLNLFL-----PVIFAMP-----ESYSFNCPDGEY---QSNDVCCKTC 53
            :|::    | |:|| | :      ||  :|     |     || |:|   |:| :||  |
Db      3 LSTVPDLLLPLVLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKC 62

Qy     54 PSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMV--ADCSATSD 111
          ||::   |  |     | :|  |:||  :| |  |  || | |:   |  : |:   |
Db     63 HKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRD 122

Qy    112 RKCECQIGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 156
          | |:   | :|  :    |  |: |  |  |   |    ||||:
Db    123 TVCGCRKNQYRHYWSENLFQCFNCSLCLNG-TVHLSCQEKQNTVCT 167


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